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APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718P2C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1992-05-07
PRIOR FILING DATE: 1991-08-14
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/252-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 amino acids
TYPE: Amino Acid
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Patent No. 6329509
GENERAL INFORMATION:
                                    NUMBER OF SEQ ID NOS:
SEQ ID NO 8
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Best Local Similarity
LENGTH: 453
TYPE: PRT
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ilarity 58.9%;
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Pred. No. 9.1e-90;
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                                                                                         NUMBER OF SEQ ID NOS:
SEQ ID NO 8
LENGTH: 453
TYPE: PRT
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Best Local Similarity 58.9%;
Matches 271; Conservative 2
                                                                                                                                                                         APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amender FILE REFERENCE: P0718P2C3US
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US/09/802,096
CURRENT FILING DATE: 1995-03-15
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/105,899
PRIOR APPLICATION NUMBER: US 08/105,899
PRIOR APPLICATION NUMBER: US 08/105,899
PRIOR FILING DATE: 1994-01-26
PRIOR FILING DATE: 1992-08-14
PRIOR FILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF THE NOCE 1991-08-14
NUMBER OF THE NOCE 1991-08-14
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                                           ORGANISM: Artificial sequence FEATURE:
                     OTHER INFORMATION:
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Pred. No. 9.1e-90;
                     version
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Query Match

46.68;

Score

BB

Length 453;

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RESULT 59
US-08-378-939-10
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Patent No. 5
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                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
APPLICATION NUMBER: US 07/952640
APPLICATION INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 103-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                        STREET: 555 THIRT:
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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5876961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS------QL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
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555 THIRTEENTH
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TH ST. N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Sequence 8, Application US
Patent No. 6113898
GENERAL INFORMATION:
APPLICANT: Anderson, D
TITLE OF INVENTION: "M
TITLE OF INVENTION: "M
TITLE OF INVENTION: DH
TITLE OF INVENTION: IN
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                                                                                                                          COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATCHITIN Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,550

PTTTYNO NAME 07-IMM-1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
     ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.6%;
Local Similarity 66.2%;
les 258; Conservation
                                                                                                   FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                             CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               446
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                                                                                                                                                                                                                                                                                                                                 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                BURNS, DOANE,
703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                    IMMUNOSUPPRESANTS"
                                                                                                                                                                                                                                                                                                                                                                                                                   "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08487550
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Pred. No. 9.8e-
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                SWECKER & MATHIS
                                  012712-131
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USE THEREOF
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; INFORMATION FOR SEQ ID NO: (
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-550-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 61
US-09-526-098-8
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Best Local Similarity
Matches 259; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Anders
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Anderson, D
TITLE OF INVENTION: "M
TITLE OF INVENTION: PH
TITLE OF INVENTION: IM
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
FILING DATE: US 08/487,550 FILING DATE: 07-JUN-1995
                                                                                                         FILING DATE:
                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                      COUNTRY: US
ZIP: 22314
                                                                                                                                                                                                                                                                                                           CITY: Alexandria
                                                      APPLICATION NUMBER:
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Query Match Best Local S Matches 274

Similarity

46.6%;

Conservative

30;

Score 1258.5; DB 4; Pred. No. 1.1e-89; 0; Mismatches 85;

Length

91;

; ORGANISM: Homo sapiens US-09-499-846-10

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RESULT 62
US-09-499-846-10
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                                                                                     GENERAL INFORMATION:
APPLICANT: KAVANAUGH et al.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN
FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILLING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 10
LENGTH: 497
TYPE: PRT
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TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
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                                                                                                                                                                                                                      Sequence 10, Application US/09499846 Patent No. 6656728
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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APPLICANT: Kavanaugh et al.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION
FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASUSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 525
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Best Local Similarity
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-----APEPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 251
                                                                                                                                                                                                                                                                                       KLHAVPÄA-----KTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA 120
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                                                                                                        --QGGKTLSVSQLELQDSGTWTC-----TVLQNQKKVBFKIDIVPCP---
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                                                                         TDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLE---ALEERPAVMTSPLYL
                                                                                                                                           AGLPÄNKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNT
                                                                                                                                                                                                                   TWSIIMDSVVPS-----
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                                                                                                                                                                                                                                                                                                                                                           46.6%; Score 1258.5; DB 4; 57.1%; Pred. No. 1.2e-89; ative 30; Mismatches 85;
                                                                                                                                                                                                                   -----DKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----DKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQ
                                                                                                                                                                                -GSS-----PSVQCRSPRGKNI 163
                                                                                                                                                                                                                                                                                                                                                           Indels
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US-08-887-352B-14
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Matches
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Patent No. 5994511
GEMERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leona:
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy di

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFFMARE: WinDatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,352B

FILING DATE: 03-Jul-1997

CLASSIFICATION: 530

CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Henry B. Low TITLE OF INVENTION: Imp TITLE OF INVENTION: IMP TITLE OF SEQUENCES: 26 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: South San
STATE: Californi
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----
                                                                                                                                                     SRDDSKNTFYLOMN-----SLRAEDTAVYYCARGSH-----YFG-----HWHFAV
                                                                                                                                                                                           DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH----LL 134
                                                                                                                                                                                                                                LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNYNPSVKGRITI 70
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VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC
                                     ----QLELQDSG----
                                                                        WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
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- can Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Improving Polypeptides
                                                                                                                                                                                                                                                                                                                         46.5%; Score 1257; DB 2;
58.4%; Pred. No. 1.3e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lowman, Leonard G. Presta, Paula M. Jardieu, Improved Anti-IgE Antibodies and Method of
                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P1123
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                                     ----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
                                                                                                                                                                                                                                                                                                                                            Length 451;
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US-08-887-352B-16
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Best Local :
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Patent No. 599451
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APPLICANT: Henry
                                                                                                                                                                                                                                                                          TYPE: Amino Acid
TOPOLOGY: Line
887-15
                                                                                                                                                                                                                                                                                                                                                                                          NAME: SVODOdA, CRAIG G.
REGISTRATION NUMBER: 39,044
REFERENCE DOCKET NUMBER: P1:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb /
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/OFILING DATE: 03-Jul-1997
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                                                                                                                78 DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH---LL
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                                                                                                                                                                             30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLN------
                                                                                                                                                                                                                           Similarity
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                                                        QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------
                                                                                      SRDDSKNTFYLOMN-----SLRAEDTAVYYCARGSH-----YFG-----HWHFAV 110
                                                                                                                                                 LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNYNPSVKGRITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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 ---QLELQDSG--
                            WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
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                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genentech, Inc
                                                                                                                                                                                                                           46.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lowman, Leonard G. Presta, Paula M. Jardieu, Improved Anti-IgE Antibodies and Method of Improving Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/887,352B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.44 Mb floppy
                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                           P1123
                                                                                                                                                                                                                         Score 1257; DB 2;
Pred. No. 1.3e-89;
                                                                                                                                                                                                              Mismatches
-TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC 210
                                                                                                                                                                                                                                         Length 451;
                                                                                                                                                                                                           Indels
                                                         --KTLSVS-----
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RESULT 66
US-08-466-151-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 6037453
GENERAL INFORMATION:
                                                                     TELEFAX: 650/952-9881 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                           FILING DATE: 07-MAY-PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8:
FILING DATE: 07-MAY-1992
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/40
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/10
FILING DATE: 26-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/4
FILING DATE: 06-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1 L. STREET: South San Fra CITY: South San Fra California
                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jardieu, APPLICANT: Presta, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: (
                                                                                                                                        NAME: Syoboda, Craig G. REGISTRATION NUMBER: 39,044 REFERENCE/DOCKET NUMBER: PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                LENGTH:
                                                                                                      TELEPHONE:
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650/952-9881
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Sequence 14, Application US/09109207C

Sequence 14, Application US/09109207C

Patent No. 6172213

GENERAL INFORMATION: Improved Anti-Ige Antibodies and Method of Improved ITILE OF INVENTION: Improved Anti-Ige Antibodies and Method of Improverille Reference: P1123R1

CURRENT APPLICATION NUMBER: US/09/109,207C

CURRENT APPLICATION NUMBER: US/09/109,207C

CURRENT FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/051,554

PRIOR APPLICATION NUMBER: US 60/051,554

LENGTH: 451

LENGTH: 451
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US-09-109-207C-14
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Best Local S
Matches 272
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                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial
LOCATION: 1-451
OTHER INFORMATION: Heavy chain sequence derived
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QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----
                           SRDDSKNTFYLOMN-----SLRAEDTAVYYCARGSH-----YFG-----HWHFAV 110
                                                                                       LVQPGGSLRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNYNPSVKGRITI
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                                                        DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH---LL 134
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                                                                                                                                              Score 1257; DB 3;
Pred. No. 1.3e-89;
5; Mismatches 79;
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LILLE OF INVENTION: Improved Anti-IgE Antibodies and FILE REFERENCE: P1123R1; CURRENT APPLICATION NUMBER: US/09/109,207C; CURRENT FILING DATE: 1998-06-30; PRIOR APPLICATION NUMBER: US 60/051,554; PRIOR APPLICATION NUMBER: US 60/051,554; PRIOR FILING DATE: 1997-07-03; NUMBER OF SEQ ID NOS: 44

SEQ: ID NO 16; LENGTH: 451

LENGTH: 451

TYPE: DDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-109-207C-16
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KBY: Artificial
LOCATION: 1-451
OTHER INFORMATION: Heavy chain sequence derived from MAE11
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ORGANISM: Artificial
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GVEVHNAKTKPREEGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                      DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                                                                                                              WGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG 170
                                                                                                                                                                                                                                                                      QGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----
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                                                                 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
                                                                                                                                               VHTFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC
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; Pred. No. 1.3e-89;
25; Mismatches 79
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US-09-296-005-14
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Pa
APPLICANT: Henry B. Lowman, Leonard G. Presta, Pa
TITLE OF INVENTION: Improved Anti-IgE Antibodies
FILE REFERENCE: P1123C1r
CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US/08/887,352
EARLIER FILING DATE: 1997-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 272; Conserv
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ORGANISM: Artificial
FEATURE:
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                                                                                                                                           GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
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Pred. No. 1.3e-89;
S; Mismatches 79;
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                                 US-09-920-171-14
                                               RESULT 71
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu,
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of In
FILE REFERENCE: P1123Clr
CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER FILING DATE: 1997-07-02
Sequence 14, Application US/09920171 Patent No. 6682735
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LENGTH: 4'51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Artificial LOCATION: 1-451 OTHER INFORMATION: Heavy chain
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Pred. No. 1.3e-89;
5; Mismatches 79
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APPLICANT: Lowman, Henry B.

APPLICANT: Presta, Leonard G.

APPLICANT: Paresta, Leonard G.

APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-IgE Antibodies (a., FILE REFERENCE: P1123C2US
CURRENT APPLICATION NUMBER: US/09/920,171
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR FILING DATE: 1997-07-02

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GENERAL INFORMATION:

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; OTHER INFORMATION: Heavy chain sequence derived
US-09-920-171-14
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US-09-920-171-16
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                                                                                                                            APPLICANT: Lowe, John
TITLE OF INVENTION: Improved Anti-IgE Antibodies (as
FILE REFERENCE: PII-3CZUS
CURRENT APPLICATION NUMBER: US/09/920,171
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: US 08/887,352
PRIOR FILING DATE: 1997-07-02
PRIOR FILING DATE: 1997-07-02
PRIOR FILING DATE: 1999-04-21
NUMBER OF EQ ID NOS: 44
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; OTHER INFORMATION: Heavy chain sequence derived US-09-920-171-16
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PRIOR FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 14
LENGTH: 451
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application Patent No. 6682735
                                                                                            SEQ ID NO 16
LENGTH: 451
                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                      APPLICANT: Lowman, Henry B.
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
APPLICANT: Lowe, John
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ORGANISM: Artificial Sequence
                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NKPSNTKVD----KKVEPKSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC
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Best Local Similarity
Matches 272; Conservat
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                                                                                                                                              GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
                                                                                                                                                                                                              DKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                  DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                            GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
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                                                                                                                                                                                          DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
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; Pred. No. 1.3e-89;
25; Mismatches 79;
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                                 431
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RESULT 73
US-08-793-450-8
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                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9-
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: EDELMAN, LENA
APPLICANT: MARCARITTE, CHRISTEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHAABIHI, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS
TITLE OF INVENTION:
                                                                                                                                                                                   COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS ADDRESSEE: OBLON, SI ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                           STREET: 1755 SO
CITY: ARLINGTON
STATE: VA
                                                                                                                                         APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
REGISTRATION NUMBER:
                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                    SOUTH JEFFERSON
                                                                                  FR 94/10566
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                                                                                                                                                                                                               Version
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Sequence 43, Application US/09301593A

Patent No. 6455677

GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Bamberger, Uwe
APPLICANT: Heger, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Seldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
FILE REFERENCE: 0652.1890001

CURRENT APPLICATION NUMBER: US/09/301,593A

CURRENT APPLICATION NUMBER: US/09/301,593A

CURRENT APPLICATION NUMBER: EP 98107925.4

EARLIER FILING DATE: 1998-04-30

EARLIER FILING DATE: 1998-04-30

EARLIER FILING DATE: 1998-05-18

NUMBER OF SEQ ID NOS: 108

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 43

LENGTH: 472

TYPE: PRT
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US-09-301-593-43
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Best Local Similarity 59.0%;
Matches 268; Conservative 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTQTCPPCPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKSRWOOGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSKNQFSLKLNSVTAADTAVYYCARAPE-----YKWKYHGDWFDPWGQGTTVTVSSA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESP 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEQYNSTYRVVSVLKVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 317
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Pred. No. 1.4e-89;
5; Mismatches 93;
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RESULT 75
US-09-289-942A-7
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                                                                                                                                                                                                                                US-09-289-942A-7
                                                                                                                                                                                                                                                                                                    APPLICANT: Pai, Emil F.
APPLICANT: Klein, Michel H.
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Pedyczak, Arthur
TITLE OF INVENTION: Fab'-EBITOPE COMPLEX FROM THE HIV-1 CROSS-NEUTRALIZING
TITLE OF INVENTION: MONOCLONAL ANTIBODY 2F5
FILE REFERENCE: 1038-926 MIS:jb
CURRENT APPLICATION NUMBER: US/09/289,942A
CURRENT FILING DATE: 1999-04-13
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09289942A Patent No. 6482928
GENERAL INFORMATION:
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Best Local Similarity
Matches 273; Conserv
                                                                                                                                                     Matches
                                                                                                                                                                     Query Match 46.4%;
Best Local Similarity 66.2%;
                                                                                                                                                                                                                                                                  LENGTH: 462
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                ORGANISM: Human immunodeficiency virus type
 138
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                                 151 PSVQCRSPRGKNIQGG--
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                                                                                                                                                     258;
                                                                                                             94 LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGL-TANSDTHLLQ--GQSLTLTLESPPGSS
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PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALPAPIEKTISKAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGY---DEGHAMDYWGQGTLVTVSSST-KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKTSRYTFTEYTIHWVRQAPGQRLEWIG--
                                                                           LVMTRVSPVDTATYFC----AHRRGPTTLFGVPIARGPVNAMDVWGQGITVTISSASTKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GINPNNGIPNYNOKFKGRATLTVGKSASTAYMELSSLRSEDTAVYYC-----ARRRIA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSFLTKGPSKLNDRADSRRSLW----DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----QLELQDSG-------TWTCTVLQNQKKVEFK 196
                                                                                                                                                     18;
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                                                                                                                                                 Score 1255; D
Pred. No. 1.9e
18; Mismatches
                                     --KTLSVS----
                                                                                                                                                                         .9e-89;
                                                                                                                                                                                         DB 4;
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                                                                                                                                                                                       Length 462;
                                                                                                                                                     Indels
                                   ----QLELQDSG----
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Sequence 2, Application US/09679397

Patent No. 6339142

GENERAL INFORMATION:

APPLICANT: BASEY, CAROL D.

APPLICANT: BLANK, GREG S.

TITLE OF INVENTION: PROTEIN PURIFICATION

FILE REFERENCE: P1241R1D2

CURRENT APPLICATION NUMBER: US/09/679,397

CURRENT FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: US 60/084,459

PRIOR APPLICATION NUMBER: US 09/304,465

PRIOR APPLICATION NUMBER: US 09/304,465

PRIOR APPLICATION NUMBER: US 09/304,465

PRIOR PILING DATE: 1999-05-03
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US-09-679-397-2
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SEQ ID NO 2
LENGTH: 449
TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                  Query Match 46.4%; Score 1254.5; D. Best Local Similarity 57.8%; Pred. No. 2e-89; Matches 268; Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 THTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267
                                                                                                                            172 TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK
                                                                                                                                                          173 --QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                                                                                                                                                                                             112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
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                                                                                                                                                                                                                                                          66 GRFTISADTSKNTAYLQMNSLRAEDTAVYYC------SRWGGDGFYAMDYWG 111
                                                                                                                                                                                                                                                                                                                   11 LVQPGGSLRLSCAASGFNIKDTYIHW-----VRQAPGKGLEWVARIYPTNGYTRYADSVK 65
                                                                                                                                                                                                                                                                                                                                               30 LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQG-----SFLTKGPSKLNDRAD
                                                                                                                                                                                                                                                                                        82 SRRSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--G 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS------ 172
                                                                                                                                                                                           QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 171
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 449;
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                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                     87; Gaps
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дь <i>1</i>	ov da Vo	Qy Db	Qy db	ОУ	Db Qy	Qy Db	Qy db	Query Ma Best Loc Matches	Db RESULT 77 RESULT 77 US-09-680- Sequence Sequence Fatent N GENERAL APPLICAL APPLICAL APPLICAL APPLICAL CURRENT CURRENT CURRENT FRIOR A PRIOR B PRIOR A PRIOR B PRIOR A PRIOR B PR	Qy .
06 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG	328 PREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDG 387	268 EVHNAKTKPREEQXNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327 	213 THTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV 267	173QLELQDSGTWTCTVLQNQKKVBFKIDIVPCPAPEPKSCDK 212	137 QSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVS	82 SRRSLWDQGNFPLIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136 ; ; ; ; ; ; ; ; ; ;	30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRAD 81	46.4%; Score 1254.5; DB 4; Length 449; Local Similarity 57.8%; Pred. No. 2e-89; hes 268; Conservative 30; Mismatches 79; Indels 87; Gaps 12;	346 ii 388 S 388 S 406 S 100 S	28 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG

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RESULT 79
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APPLICANT: BLANK, GREG S.
TITLE OF INVENTION: PROTEIN PURIFICATION
FILE REFERENCE: P1241R1
CURRENT APPLICATION NUMBER: US/09/304,465A
CURRENT FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/084,459
PRIOR FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 2
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LENGTH: 449
TYPE: PRT
                                                                                                                                                                             Sequence 4, Application US/08487550 Patent No. 6113898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION:
Patent No. 6489447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Applicat Patent No. 6489447 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                           GENERAL INFORMATION:
                                                    APPLICANT: Anderson, I
TITLE OF INVENTION: TO
TITLE OF INVENTION: TO
TITLE OF INVENTION: PH
TITLE OF INVENTION: IN
NUMBER OF SEQUENCES: 1
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE,
STREET: 699 Prince Street
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                                                                                                                                                                                                                                                                                                                    388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRFTISADTSKNTAYLOMNSLRAEDTAVYYC-----SRWGGDGFYAMDYWG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRRSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--G 136
                                                                                                                                                                                                                                                                                   SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----
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"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND
                                                                        IMMUNOSUPPRESANTS"
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Pred. No. 2e-89;
30; Mismatches
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                     & MATHIS
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; Sequence 4, Application US; Patent No. 6492134; GENERAL INFORMATION: APPLICANT: Anderson, ITILE OF INVENTION: "NO. TITLE OF INVENTION: TX;

, Darrell R. "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED F

FORMS

RESULT 80 US-09-526-098-4

US/09526098

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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 1476 amino acids
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TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/487,550 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
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REGISTRATION NUMBER:
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TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
                                                                                    LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
                                                                                                                                                      PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
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Pred. No. 7e-89;
6; Mismatches
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US-09-526-098-4
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: IN
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                              LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
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699 Prince Street
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US-08-472-888A-7
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; ORGANISM: Homo
US-09-313-942-9
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CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
NUMBER OF SEQ ID NOS: 32
GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Walz, Gerd
TITLE OF INVENTION: AGE
TITLE OF INVENTION: AND
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09313942
Patent No. 6472179
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
TITLE OF INVENTION: AND USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows SEQ ID NO 9
                                                                                                                      Sequence 7, Application US/08472888A Patent No. 6613746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 TKGPSKLNDRADSRRSL--WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQ------
                                                                                                                                                                                                                                                                                                                                                      LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
                                                                                                                                                                                                                                                                MHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                               VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -------LLVFGLTANSDTHLLQGQSLTLTL-----ESPPGSS---PSVQCRSPRGK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKGPTVRTKKVGKNEAVLEWDQ--LPVDVQNGFIRNYTIFYRTIIGNETAVNVDSSHTEY
                                                                                                                                                                                                                                                                                                                          LVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
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  AGP-ANTIBODY FUSION PROTEINS AND RELATED MOLECULES AND ME: 9
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DB 4; 66;

Indels Length 951;

85;

Gaps

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412

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811 292 751 232

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RESULT 83
PCT-US96-10043-9
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Sequence 9, Application PC/TUS9610043
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IN COMPATIBLE
COMPUTER: IN COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,888A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/618,314
FILING DATE: 23-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 00786/258001
TELECHONG: 617-428-0200
TTELEPHONG: 617-428-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 74.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acids
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CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
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                                                                                                                                                                                                                                                                                        RDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 399
                                                                                                                                                                                                                                                                                                                                                                                                                                         LGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 181
                                                                                                                                                                                                                           SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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176 Federal Street
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Pred. No. 3.8e-88;
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Best Local Similarity
Matches 246; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acids
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REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TELEFAX: 200154
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CITY: Boston
STATE: MA
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CTREST: 225 Franklin Street
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CLASSIFICATION:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US96/10043
410
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                                                                                                                                                                                                                                                                                           173 ---QLELQDSGTWTCTVL-----QNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PEL
                                                                                                                                                                                                                                                                                                                           122 GOGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
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SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                    SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                           RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
                                                                                            RDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDK 399
                                                                                                                              QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                               QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                              LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
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Pred. No. 3.8e-88;
2; Mismatches 26
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                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
441
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US-09-746-359A-54 RESULT 84

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289

349

409

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229 219 181

Sequence 54, Application US/09746359A Patent No. 6610286 GENERAL INFORMATION: APPLICANT: Thompson, Penny APPLICANT: Foster, Donald C.

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US-09-746-359A-53
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SEQ ID NO 54
LENGTH: 547
TYPE: PRT
ORGANISM: Homo sapiens
US-09-746-359A-54
                                                                                                                                                                                             RESULT 85
                                                          Sequence 53, Application US/09746359A
PATENT NO. 6610286
GENERAL INFORMATION:
APPLICANT: Thompson, Penny
APPLICANT: Foster, Donald C.
APPLICANT: Xu, Wenfeng
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Best Local Similarity
         APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/171,969
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/213,341
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: No. 6610286ak, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108
                                                                                                                                                                                                                                                                                                                                                                                               378
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Madden, Kart...
Kelly, James D.
Chrecher, Cindy P
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Kelly, James D.
Sprecher, Cindy A.
Blumberg, Hal
Eagan, Maribeth A.
Jaspers, Stephen R.
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                                                                                                                                                                                                                                                                                                                       KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
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                                                                                                                                                                                                                                                 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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58.8%;
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Pred. No. 5.le-88;
3; Mismatches 72; Indels 9
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RESULT 86 US-08-236-311-7

Sequence 7, Application US/08236311

Fatent No. 5565335

GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants

NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,

STREET: 460 Point San Bruno CITY: South San Francisco

Blvd

STATE: C

California

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APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: Chandrasekher, Yasmin A.
APPLICANT: No. 6610286ak, Julia E.
TITLE OF INVENTION: Method for Treating Inflammation
FILE REFERENCE: 99-108
CURRENT APPLICATION NUMBER: US/09/746,359A
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 60/171,969
PRIOR APPLICATION NUMBER: 60/171,969
PRIOR APPLICATION NUMBER: 60/213,341
PRIOR APPLICATION NUMBER: 60/213,341
PRIOR FILING DATE: 2000-06-22
NUMBER: 710 NOC. 72
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SEQ ID NO 53
LENGTH: 571
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 45.8%;
Best Local Similarity 58.8%;
Matches 276; Conservative 2
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APPLICANT:
APPLICANT:
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522
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                                                                                                                                                                                                                                                                                                                                                                                                                                             134 LQGQSLTLTLESPPGSS--PSVQCRSPRGKNIQGG-----KTLSVS-----
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                       LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                     KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                                                                YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLWDQ--GNFPLIIKNLKIEDSDTYICEVED-----QKEEVQLLVFGLTANSDTHL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVVLGKKGDTVELTCTASOKKSIOFHWK-NSNOIKILGNO-GSFLTKGPSKLNDRADSRR
LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                       KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                                                                                                                                                       KSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
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                                                                           KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                                           YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                                                                                                             -----QLELQDSG-------TWTCTVLQNQKKVEFKIDIVPCPAPEP
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Eagan, Maribeth A.
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; Pred. No. 5.4e-88;
23; Mismatches 72;
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                                                                                                US-08-457-918-7
Sequence 7, Application US/08457918
Patent No. 6117655
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
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FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION NUMBER: 07/104329
PRIOR APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
APPLICATION NUMBER: 08/164
REFERENCE/DOCKET NUMBER: 444P1C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/255-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
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MEDIUM TYPE: 5.25 inch, 360 Kb f
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                      GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 370
                                                                                                                                                                                           GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                              QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD
                                                                                                                                                                                                                                                                     QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD 386
                                                                                                                                                                                                                                                                                                                       VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
                                                                                                                                                                                                                                                                                                                                          VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG 326
                                                                                                                                                                                                                                                                                                                                                                                               KTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG
                                                                                                                                                                                                                                                                                                                                                                                                                      KTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.8%;
72.2%;
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Pred. No. 3.9e-88;
9; Mismatches 32; Indels 55;
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                                                                                                                                                                                                                                                                                                                                                                                                               Matches 249;
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 45.8%;
Best Local Similarity 72.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: SEQUENCE: 371 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P044
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/236:
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA: 07/936:
APPLICATION NUMBER: 07/936:
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/842:
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/956:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
COMPUTER: IBM PC compacti
OPERATING SYSTEM: PC-DOS
SOFTWARE: patin (Genente
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Adheson Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415/1-7168
TRLEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
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 387
                                                                         327
                                                                                                                                       267 VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
                                                                                                                                                                                    146 KTHTCPPCPAPELLGGPSVPLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG
                                                                                                                                                                                                                                                                                                173 ---QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCD
                                                                                                                                                                                                                                                                                                                                                                        136 GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----
                                                                                                                                                                                                                                                          92 HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCD
                                                                                                                                                                                                                                                                                                                                   32 GLGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV
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South San Francisco
: California
GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                  QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD
                                                          QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD
                                                                                                            VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
                                                                                                                                                                                                                         KTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG
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SYSTEM: PC-DOS/MS-DOS
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Bruno
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Pred. No. 3.96
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG

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RESULT 89
US-09-590-656-2
; Sequence 2, Application US/09590656
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; ORGANISM: Homo sapiens
US-09-157-452B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/157,452B
CURRENT FILING DATE: 1998-09-21
PRIOR APPLICATION NUMBER: US 08/950,660
PRIOR FILING DATE: 1997-10-15
PRIOR APPLICATION NUMBER: US 08/373,857
PRIOR FILING DATE: 1995-01-18
PRIOR FILING DATE: 1995-01-18
PRIOR APPLICATION NUMBER: US 08/284,603
PRIOR FILING DATE: 1994-08-11
PRIOR APPLICATION NUMBER: PCT/US93/00924
PRIOR FILING DATE: 1993-02-02
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PRIOR FILING DATE: 1992-02-12
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Applica Patent No. 6482409
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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APPLICANT: Burkly, Linda C.
TITLE OF INVENTION: TREATMENT FOR INFLAMMATORY
FILE REFERENCE: 10274-004003
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                                                                                                                                      381 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 LLVFGLTANSDTHLLQGQSLTLTLESPP---GSSPSVQCRSP------RGKNI 163
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                                                                                                                                                                                                                                                                                                                  ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 380
                                                                                                                                                                                                                                                                                             NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 334
                                                                                                                                                                                                                                                                                                                                                                                   KELQVDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKSQEFLEDADRKSLETKSLEVTFTPVIEDIG----KVLVCRAKLHIDEMDSVPTVRQAV 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QGG-----KTLSVSQLE-----LQDSGTWTCTVLQNQKKVEF-KIDIVPC--PAP 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G--SFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEV--EDQKEE--VQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LWIMFAASQAFKIETTPESRYLAQIGDSVSLTCSTTGCESPFFSWRTQIDSPLNGKVTNE
                                                                                                               PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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Pred. No. 7.1e-88;
6; Mismatches 70; Indels 95;
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SOFTWARE: Patentin Ver.
SEQ ID NO 2
LENGTH: 704
TYPE: PRT
ORGANISM: Homo sapiens
US-09-590-656-2
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                                                                                                                                                                                                                                                         APPLICANT: Cerretti, Douglas P.
APPLICANT: Borges, Luis G.
APPLICANT: Borges, Luis G.
APPLICANT: Panslow, III, William C.
TITLE OF INVENTION: TEX ANTAGONISTS
FILE REFERENCE: 2900-A
CURRENT APPLICATION NUMBER: US/09/733,764
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 09/590,656
PRIOR APPLICATION NUMBER: 09/590,656
PRIOR FILING DATE: 1999-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cerretti, Douglas P.
APPLICANT: Borges, Luis G.
APPLICANT: Borges, Luis G.
APPLICANT: Fanslow, III, William C.
TITLE OF INVENTION: TEK ANTAGONISTS
FILE REFERENCE: 2900-A
CURRENT APPLICATION NUMBER: US/09/590,656
CURRENT FILING DATE: 2000-06-07
PRIOR APPLICATION NUMBER: 60/137,889
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 2
COUNTAINTE: BECAUTE VOT 2 0
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Matches
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID 2
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Best Local Similarity 82.5%;
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GENERAL INFORMATION
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09733764
Patent No. 6521424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 236;
                                                                                                                                                                       LENGTH: 70
TYPE: PRT
                                                                 Local Similarity
nes 236; Conserv
418
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                           DSGTWTCTVLQNQKKVE--FKIDIVPCPAP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKTHTCPPCPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
DSGVWVCSVNTVAGMVEKPFNISVKVLPKPLNAPNVIDTGHNFAVINISSEPYFGEPKSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
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                                                                 45.6%; ilarity 82.5%; Conservative
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4; Mismatches 14
                                                                 Score 1232; DB 4;
Pred. No. 2.1e-87;
4; Mismatches 14;
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Pred. No. 2.1e-8
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                                                                   14;
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                                                                   Indels
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US-08-461-968A-5
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                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                          TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                        CLASSIPICATION: 536
PRIOR APPLICATION NUMBER: US 07/618
PILING DATE: 23 NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELECHNONE: 617/542-570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACTION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acids
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ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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TITLE OF INVENTION: INHIBITION OF CELL ADHESION
TITLE OF INVENTION: PROTEIN-CARBOHYDRATE INTERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not rel
TOPOLOGY: linear
DLECULE TYPE: protein
                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 05-JU
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---QLELQDSGTWTCTVL----QNQKKVEFKIDIVPCPAPEPKSCDKTHTC----PEL
                                             GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
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                                                                                      GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----
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                                                                                                                       Conservative
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                                                                                                                                                                                                                                         not relevant
                                                                                                                                     45.4%;
73.5%;
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                                                                                                                   Score 1226; DB 1;
Pred. No. 3.2e-87;
.2; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Version
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                                                                                      ----KTLSVS-----
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US-08-462-571-5
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                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Seed, Brian et al.
TITLE OF INVENTION: INHIBITION OF CELL ADHESION
TITLE OF INVENTION: PROTEIN-CARBOHYDRATE INTERACTIONS
                                                                                                                                                                                                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PS/2 model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTWARE: Wordberfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 07/618,314
FILING DATE: 23 No. 5858983ember 1990
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                   TYPE:
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                                                                                                                                                                                                                                                                  LENGTH:
173 ---QLELQDSGTWTCTVL-----QNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PEL
                                    122 GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 181
                                                                     136 GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------
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Pred. No. 3.2e
L2; Mismatches
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PCT-US96-10043-11
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TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
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GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 14
                                                                                                                                                           Query Match
                                                                                                                 Matches
                                                                                                                                      Best Local Similarity
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MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10043
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 00786/284001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5970
TELEPAX: 617/542-8906
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,213
FILING DATE: 14-JUN-1995
CLASSIFICATION:
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ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                  STRANDEDNESS: not
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                       120 LILRDTKTYMLAFDVNDEKN-----WGLSVYADKPETTKEQLGEFYE-----ALDCL 166
                                                                  99 LKIEDSDTYIC--EVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQC- 155
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                                                                                                            45.3%; Score 1224; DB 5; Length 437;
72.3%; Pred. No. 4.5e-87;
tive 16; Mismatches 38; Indels 4
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  402 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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167 RIPK		
167 RIPK	240 EMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 2	
167 RIPK	342 ELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 4	
167 RIFK	282 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD	
167 RIPK	120 GPSVFLFPPKPKDTLMIGRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKFREEQY	
	222 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 2	
167 RIPK	181TWTCTVLQNOKKVEFKIDIVPCPAPEPKSCDKTHTCPELLG 2	
211 DKTHTC	151 PSVQCRSPRGKNIQGGKTLSVSQLELQDSG	
167 RIPK	tch 45.2%; Score 1221.5; DB 4; Length 330; :al Similarity 73.9%; Pred. No. 4.8e-87; 244; Conservative 9; Mismatches 22; Indels 55; Gaps	
	EARLIER APPLICATION NUMBER: EP 98107925 EARLIER FILING DATE: 1998-04-30 EARLIER APPLICATION NUMBER: US 60/086,0 EARLIER FILING DATE: 1998-05-18 NUMBER OF SEQ ID NOS: 108 SOFTWARE: Patentin Ver: 2.0 SEQ ID NO 22 LENGTH: 330 TYPE: PAT ORGANISM: Homo sapiens -09-301-593-22	
167 RIPKSDVVYTDWKKDKCEPLEKÖHEKERKÖEEGESDPEGEPKSC 211 DKTHTCPELLGGPSVFLFPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 211 DKTHTCPPCPAPELLGGPSVFLFPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 266 GVEVHNAKTKFREEQYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAK 271 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAK 271 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAK 271 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAK 326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 331 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 332 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 333 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 340 GCPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVENSKTYPPVLDS 340 GCPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVENSKTYPPVLDS 340 GCPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVENSKTYPPVLDS 340 GCPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVENSKTYPPVLSHAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAK	ENT APPLICATION NUMBER: US/09/ ENT FILING DATE: 1999-04-29	
167 RIPKSDVVYTDWKKDKCEPLEKQHEKERKQEEGESDPBGEPKSC 211 DKTHTCPELLGGPSVFLFPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 211 DKTHTCPCPAPELLGGPSVFLFPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 211 DKTHTCPPCPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK	APPLICANT: Leger, Oliver APPLICANT: Saldanha, Jose W. APPLICANT: Rettig, Wolfgang J. TITLE OF INVENTION: FAP-specific Antibody with Improved Producibili FILE DEFERENCE. 0652 1890001	
167 RIPKSDVVYTDWKKDKCEPLEKQHEKERKQEEGESDPEGEPKSC 211 DKTHTCPELLGGPSVFLFPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 211 DKTHTCPCPAPELLGGPSVFLFPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 211 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 212 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 213 OKTHALPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 214 DKTHTCPPCPAPELLGGPSVFLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 215 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 216 GOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 326 GOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 331 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 332 GOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 333 GOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 336 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431	APPLICANT: Garin-Chesa, Pila APPLICANT: Bamberger, Uwe	
167 RIPKSDVVYTDWKKDKCEPLEKÖHEKERKÖEEGESDPEGEPKSC 211 DKTHTCPELLGGPSVFLFPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 211 DKTHTCPPCPAPPELLGGPSVFLFPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 216 GVEVHNAKTKFREEQYNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAK [Sequence 22, Application US/09301593 Patent No. 6455677 GENERAL INFORMATION:	
167 RIPKSDVVYTDWKKDKCEPLEKQHEKERKQBEGESDPEGEPKSC 211 DKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 211 DKTHTCP-PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 211 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 271 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 331 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 386 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431	SULT 94 -09-301-593-2	
167 RIPKSDVVYTDWKKDKCEPLEKOHEKERKQEEGESDPEGEPKSC 211 DKTHTCPELLGGPSVFLFPDKPKDTLMISRTPEVTCVVVDVSHEDPEVKPNWYVD 211 DKTHTCPELLGGPSVFLFPDKPKDTLMISRTPEVTCVVVDVSHEDPEVKPNWYVD 211 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK [391 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG	
167 RIPKSDVVYTDWKKDKCEPLEKQHEKERKQBEGESDPEGEPKSC 211 DKTHTCPELLGGPSVFLFPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 211 DKTHTCP-CPAPELLGGPSVFLFPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 211 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 266 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 271 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 271 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 326 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDLAVEWESNGQPENNYKTTPPVLDS 331 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDLAVEWESNGQPENNYKTTPPVLDS	386	
167 RIPKSDVYYTDWKKDKCEPLEKQHEKERKQEEGESDPBGEPKSC 211 DKTHTCPELLGGPSVFLFPDKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD	331 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS	
167 RIFKSDVVYTDWKKDKCEPLEKOHEKERKOEEGESDPEGEPKSC 211 DKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD	326 GOPREPOVYTLEPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDS 3	
167 RIPKSDVVYTDWKKDKCEPLEKQHEKERKQEEGESDPEGEPKSC 211 DKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 211 DKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 211 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 216 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK	271 GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPABIEKTISKAK 3	
167 RIPKSDVVYTDWKKDKCEPLEKQHEKERKQEEGESDPEGEPKSC 211 DKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD	266 GVEVHNAKTKDREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 32	
167 RIPKSDVVYTDWKKDKCEPLEKQHEKERKQEEGESDPEGEPKSC 211 DKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD	211 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 27	
167 RIPKSDVVYTDWKKDKCEDLEKOHEKERKOEEGESDPEGEPKSC	211 DKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD	
100 X07XG2X1CGG21E0V0CEDECE0G131C1VECNC722VD721E1V7C727D720C	156 REPKGANIQGGALISVSQUEEQQUSGINICITVAQVQTTTARVEFALIDIVECERFEFICASC	

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; SOFTWARE: FastSEQ for Win
; SEQ ID NO 8
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-8
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PCT-US95-03866-12
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                                                                                                                                                                                                                                                                                                                             Sequence 12, Application GENERAL INFORMATION
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Patent No. 6472179
GENERAL INFORMATION:
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Best Local Similarity 80.5%;
Matches 236; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR PILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS,
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
                        ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                    APPLICANT: CytoMed, Inc. (all states except US)
APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                 CITY: New York
STATE: New York
COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                             COUNTRY:
                                                                                                                                                        STREET:
                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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                                                                                                                                                                                                                                                                                                                                                     Application PC/TUS9503866
                                                                                                                                                    1251 Avenue of
                                                                                             United States of
                                                                                                                                                                          Fish & Neave
PC-DOS/MS-DOS
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Pred. No. 1.2e-86;
LO; Mismatches 22
                                                                                               America
                                                                                                                                                          Americas
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STATE: New York

COUNTRY:

United States

of America

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RESULT 97
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Sequence 14, Application PC/TUS9503866
GENERAL INFORMATION:
APPLICANT: CytoMed, Inc. (all states except US)
APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND AND
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
CORRESSORDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
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Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08 FILING DATE: 28-MAR-1994 ATTORNEY/AGENT INFORMATION: NAME: Haley Jr, James F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION TELEPHONE: 212-596-9000
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 424 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
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RESULT 98
US-09-180-100-11
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NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CytoMed/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                        Sequence 11, Application US/09180100 Patent No. 6306395
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
APPLICANT: NAKAMURA, NO. 630639510
APPLICANT: NACATA, Shigekazu
TITLE OF INVENTION: NOVEL F88 ANTIGEN DERI'
FILE REFERENCE: 1110-207P
CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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Local Similarity 66.8%;
nes 253; Conservative 1
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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; Pred. No. 1.1e-86; 
18; Mismatches 48; Indels 6
                                                                                                  DERIVATIVE
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CURRENT APPLICATION NUMBER: US/09/180,100
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: PCT/JP97/01502
EARLIER FILING DATE: 1997-05-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 376
TYPE: PRT
ORGANISM: Homo sapiens
US-09-180-100-22
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US-09-180-100-22
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; SOFTWARE: PatentIn Ver. 2.
; SEQ ID NO 11
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/09180100
Patent No. 6306395
GENERAL INFORMATION:
APPLICANT: NAKAMURA, No. 6306395io
APPLICANT: NAKAMURA, Shigekazu
TITLE OF INVENTION: NOVEL Fass ANTIGEN DERIVATIVE
FILE REFERENCE: 1110-207P
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Best Local Similarity 91.3%;
Matches 231; Conservative
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                                                                                                                                                                                                                                                                          Query Match
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Local Similarity 91.3%;
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                                                                            LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY
                                                                                                                                    SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
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PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH
                                                           LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY
                                                                                                                       SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
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Pred. No. 1.8e-86;
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Pred. No. 1.7e-86
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GENERAL INFORMATION:
APPLICANT: DEEN, KEITH C.
APPLICANT: YOUNG, PETER R.
APPLICANT: YOUNG, PETER R.
APPLICANT: WARSHALL, LISA A.
APPLICANT: MARSHALL, LISA A.
APPLICANT: TAN, KONG B.
TITLE OF INVENTION: TWOR NECROSIS FACTOR RELATED RECEPTOR,
TITLE OF INVENTION: TR6
FILE REFERENCE: GH-50008-2
CURRENT FILING DATE: 1997-06-15
PRIOR APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR APPLICATION NUMBER: 08/953,684
PRIOR APPLICATION NUMBER: 08/853,684
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR FILING DATE: 1997-03-04
INMBER OF SEQ ID NOS: 8
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 424
TYPE: PRT
GRANNISM: HOMO SAPIENS
US-09-333-593A-8
Search completed: August 3, Job time: 22.0673 secs
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US-09-333-593A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09333593A
Patent No. 6313269
GENERAL INFORMATION:
                                                                            349 SLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF 408
                                                                                                                                                                                                                                                                                                                                                                                                      168 GDCTPWSDIECVHKESGRSIEGR------GTEPKSADKTHTCPPCPAPELLGGPSVFLF
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363 NHYTQKSLSLSPG 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 EVELSPCTTTRNT---VCQCEEGTFREEDSPEMCRKCRTGCPRG------MVKV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 EVQLLVFGLTANSDTHLLQGQSLTLTLESSPGSSPSVQCRSPRGKNIQGGKTLSVSQLEL 176
                                                                                                                                                                                                                                                                                                                   PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV 288
                    2004, 13:17:18
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Result
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Maximum Match 100%
Listing first 125 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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1: /cgn2_6/ptcdata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*

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9: /cgn2_6/ptcdata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptcdata/1/pubpaa/US09A_PUBCOMB.pep:*

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2 US-10-404-724-8

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US-10-679-620-62

4 US-10-679-620-62

2 US-10-412-406-33

2 US-10-412-406-33

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Sequence 33, Appl
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Sequence 34, Appl
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19 US-10-4
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US-09-996-288-234
US-09-996-288-236
US-09-996-288-236
US-09-996-288-242
US-09-996-288-244
US-09-996-288-244
US-09-996-288-244
US-09-996-288-244
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US-09-996-288-254
US-09-996-288-254

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US-08-485-163-3
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Publication No. US20020098191A1
GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
NUMBER OF SEQUENCES:
ADDRESSEE: Cooper & Dunham LLP
                                                                                                                                                                 COUNTRY: USA

COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC_DOS/MS-DOS
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION NUMBER: US/08/485,163
FILLING DATE: 07-JUN-1995
CLASSIFICATION: 514
CULASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-1-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
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US-09-96-265-244

US-09-96-265-244

US-09-96-265-244

US-09-96-265-254

US-09-96-265-255-254

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GENERAL INFORMATION:
APPLICANT: Graham P. Allaway et al.
APPLICANT: Graham P. ANA-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJ
TITLE OF INVENTION: AND USES THEREOF
FILL REFERENCE: 2048/41215-CB/JPW/SHS
CURRENT APPLICATION NUMBER: US/99/766,995
CURRENT FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 432
TYPE: PAT
ORGANISM: homo sapians
US-09-766-995-2
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CELL TYPE:
US-08-485-163-3
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TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 405;
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Best Local Similarity
Query Match
Best Local Similarity
Matches 405; Conserv
                                                                                                                                                                                                                                                    Sequence 2, Application US/09766995
Patent No. US20020052481A1
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TOPOLOGY: unknown
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78.5%;
ilarity 91.2%;
Conservative
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lymphocyte
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91.2%;
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Score 2122; DB 9;
Pred. No. 2e-134;
8; Mismatches 5;
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Indels

26;

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Sequence 5, Application US/08485163
Publication No. US20020098191A1
GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CH
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
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US-08-485-163-5
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                                                                                                    COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER:

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,163
FILING DATE: 07-UN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 37590-II-1-PCT-US
TELECHAVUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
STATE: New York
               TYPE: amino acid
STRANDEDNESS: unl
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; ORGANISM: homo sapien
; CELL TYPE: lymphocyte
US-08-485-163-5
                                                                                                        US-09-766-995-4
                                                                                                                                                                                                                                                                                                                                   RESULT 4
                                                                                                                                                      Sequence 4, Application US/09766995
Patent No. US20020052481A1
GENERAL INFORMATION:
APPLICANT: Graham P. Allaway et al.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONTITLE OF INVENTION: AND USES THEREOFFILE REFERENCE: 2048/41215-CB/JPW/SHS
CURRENT APPLICATION NUMBER: US/09/766,995
CURRENT FILING DATE: 2001-01-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Version 3.0
SEQ ID NO 4
                                                    Query Match
Best Local S
Matches 409
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Best Local Similarity 77.3%;
Matches 409; Conservative
                                                                                                                  LENGTH: 530
TYPE: PRT
ORGANISM: homo sapians
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                                                                  Local Similarity
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                                                     Conservative
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                                                                77.2%;
                                                  9;
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Pred. No. 7.9e
9; Mismatches
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                                                               Score 2085; DB 9;
Pred. No. 7.9e-132;
                                                     Mismatches
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RESULT 5
US-09-939-537-33
US-09-939-537-33
, Sequence 33, Application US/09939537
, Publication No. US20030138410A1
, Publication No. US20030138410A1
; GENERAL INFORMATION:
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                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284,391
FILING DATE: 02-Aug-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/865,961
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/865,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KOlanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW
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                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----KSCDKTHTCP-ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 176 Federal Street
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                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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Banapour, Babak
Romeo, Charles
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-404-724-8
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US-10-404-724-8
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/10404724
Publication No. US20030203447A1
GENERAL INFORMATION:
APPLICANT: Horwitz, Arnold H.
TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.2 SEQ ID NO 8
                                                                                                                                                     Query Match 47.8%;
Best Local Similarity 58.1%;
                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 249;
                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 13698US01
CURRENT APPLICATION NUMBER: US/10/404,724
CURRENT FILING DATE: 2003-03-31
                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/368,530 PRIOR FILING DATE: 2002-03-29 NUMBER OF SEQ ID NOS: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 260
                                                                                                                                   286;
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                                 67
64 LKWMGWINTYTEEPTYGDD------FKGRFAFSLETSASTANLQINNLKSEDTATYF 114
                                                                                                  11 LLVLQLALLPAATQGNKVVLG----KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                              ----SFLTKGPSKLNDRADSRRSLWDQGNFP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 254 amino acids TYPE: amino acid
                                                                 LLFLMAAAQSAQAQIQLVQSGPELKKPGETVKISCKAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQDGELDGLWTTDP
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                                                                                                                                   Conservative
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                                                                                                                                  Score 1291.5; DB 14
Pred. No. 1.4e-78;
Pred. No. 1.7e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1338.5; DB Pred. No. 4.7e-82;
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                                                                                                                                                                       DB 12; Length 465;
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                                                                   ---GYTFTKYGMNWVKQAPGKG
                                                                                                                                     Indels 105;
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                                 ----LIIKNLKIEDSDTYI 108
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APPLICANT: Large Scale Biology
APPLICANT: Reinl, Stephen J.
APPLICANT: Rewards, Patricia C.
TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
FILE REFERENCE: 34150-004A
CURRENT PILING DATE: 2003-10-03
CURRENT FILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: 60/415,940
PRIOR APPLICATION NUMBER: 60/415,940
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 64
LENGTH: 713
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FEATURE: THEOREMATION: PREFIGERIAL SECTION 150
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US-10-679-620-64
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 Local Similarity
                                173
                                                                                                      137
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                                                                                                                                                                           77
TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKSCDK
                                                                                                                                                                                                                                           LGKKGDTVELTCTAS-------OKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL
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                                                                 QASVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
                                                                                                                                     KGRFTISRDN-DKNALYLOMNSLKSEDTAMYYC----ARRSEFYYYGNTYYYSAMDYWG
                                                                                                                                                                    NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-----ARFGSAVD-----YWGQGTSVTVSSASTKGPSVFPLAPSSKSTSGGTA
                                --QLELQDSG-----
                                                                                                    QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----
                                                                                                                                                                                                        LVKPGGSLKLSCAASGFTFSHYGMSWVRQTPDKRLEW-----VATIGSRGTY-THYPDSV 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYTOKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
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                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                47.7%;
59.3%;
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                                                                                                                                                                                                                                                                               28; Mismatches
                                                                                                                                                                                                                                                                        Score 1289; DB 10,
Pred. No. 3.6e-78;
                               ----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----QLELQDSG-----
                                                                                                                                                                                                                                                                                                              Length 713;
                                                                                                                                                                                                                                                                               Indels 80;
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Sequence 62, Application US/10679620

Publication No. US20040110930A1

GENERAL INFORMATION:
APPLICANT: Large Scale Biology
APPLICANT: Edwards, Patricia C.
APPLICANT: Edwards, Patricia C.
FITTLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
FILE REFERENCE: 34150-004A
CURRENT APPLICATION NUMBER: US/10/679,620
CURRENT FILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: 60/415,940
PRIOR FILING DATE: 2003-10-03
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.2
SEQ ID NO 62
LENGTH: 715
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local (
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                                                                                                                                              491
                                                                                                                                                                                                                  437 TFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKSCDK
                                                                                                                                                                                                                                                      173 -- QLELQDSG-------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK
                                                                                                                                                                                                                                                                                                                                                                                                                                       269 LVKPGGSLKLSCAASGFTFSHYGMSWVRQTPDKRLEW---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 LGKKGDTVELTCTAS-------QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL
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PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
                                                                     EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                          EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                                                             THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                 THTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                                                            QGASVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
                                                                                                                                                                                                                                                                                                                             QSLTLTLESPPGSSPSVQCRSPRGKNIQGG------
                                                                                                                                                                                                                                                                                                                                                                 KGRETISRDN-DKNALYLQMNSLKSEDTAMYYC----ARRSEFYYYGNTYYYSAMDYWG
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ilarity 59.3%;
Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1289; DB 16;
Pred. No. 3.7e-78;
8; Mismatches 81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 715;
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                                   387
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RESULT 10
US-10-412-406-32
US-10-412-406-32
; Sequence 32, Application US/10412406
; Publication No. US20040058394A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
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US-10-363-427-14
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CURRENT APPLICATION NUMBER: US/10/363,427
CURRENT FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 52
SOFTWARE: KopatentIn 1.71
SEQ ID NO 14
LENGTH: 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 273; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/10363427 Publication No. US20030195338A1
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APPLICANT: LEE, Hye Ja
APPLICANT: CHOI, Eun Yong
APPLICANT: KIM, Jin Mi
APPLICANT: YIM, Soo Bin
TITLE OF INVENTION: Concatametric Immunoadhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MeDexGen Inc.
APPLICANT: CHUNG, Yong Hoon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWT-----CTVLQNQKKVE
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                                                                                                                                                                                                                     GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
                                                                                                                                                                   PG 431
                                                                                                                                                                                                                                                                  NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CEVMNGTDPELNL-----YQDGKHLKLSQRVI--THKWTTSLSAKFKCTA-GNKVSKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IIKNLKIEDSDTYICEVEDQK-EEVQLLVFGLTANSDTHLLQGQ-----SLTLT 142
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                                                                                                                                                                                                   GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
                                                                                                                                     436
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PRIOR APPLICATION NUMBER: 60/240,285
PRIOR FILING DATE: 2000-10-13
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/275,289
PRIOR APPLICATION NUMBER: 60/299,987
PRIOR APPLICATION NUMBER: 60/299,987
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: PCT/US01/32140
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 33
SOPTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 663
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; ORGANISM: Homo
US-10-412-406-32
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CURRENT APPLICATION NUMBER: US/10/412,406
CURRENT FILING DATE: 2003-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LYNE, Paul
APPLICANT: SALDHANA, JOSE W.
TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R
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 618
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                       DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                            GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                      GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
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DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                         GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
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Pred. No. 5.7e-78;
9; Mismatches 71; I
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RESULT 11

US-10-412-406-33

Sequence 33, Application US/10412406

Publication No. US20040058394A1

GENERAL INFORMATION:

APPLICANT: BIOGEN, INC.

APPLICANT: GARBER, Ellen

APPLICANT: LYNE, Paul

APPLICANT: SALDHANA, Jose W.

TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTI
FILE REFERENCE: BINALOCN

CURRENT APPLICATION NUMBER: US/10/412,406

CURRENT FILING DATE: 2003-04-10

ANTIBODIES

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APPLICANT: Link, Brian

APPLICANT: T80, J Yun

TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST CD:
FILE REFERENCE: 05882-0176-CNUS04

CURRENT APPLICATION NUMBER: US/10/435,299

CURRENT FILING DATE: 2003-05-09

PRIOR APPLICATION NUMBER: US 09/618,380

PRIOR FILING DATE: 2000-07-18

PRIOR APPLICATION NUMBER: US 08/397,411

PRIOR APPLICATION NUMBER: US 08/397,411

PRIOR APPLICATION NUMBER: US 07/859,583

PRIOR APPLICATION NUMBER: US 07/859,583

PRIOR FILING DATE: 1992-03-27

NUMBER OF SEQ ID NOS: 14
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US-10-435-299-7
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; ORGANISM: Homo
US-10-412-406-33
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SEQ ID NO 33
LENGTH: 4852
                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/10435299 Publication No. US20040052783A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 275; Conserv
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PRIOR FILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/299,987
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: PCT/US01/32140
PRIOR FILING DATE: 2001-10-12
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APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
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FILING DATE: 2000-10-13
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59.0%; Pred. No. 7e-7
ative 29; Mismatches
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; TITLE OF INVENTION: Concatametric Immunoadhu
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/363,427
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 18
; LENGTH: 617
; TYPE: PRT
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                                                                                                                                                                APPLICANT: MeDexGen Inc.
APPLICANT: CHUNG, Yong Hoon
APPLICANT: HAN, Ji Woong
APPLICANT: LEE, Hye Ja
APPLICANT: CHOI, Eun Yong
APPLICANT: KIM, Jin Mi
APPLICANT: XIM, Soo Bin
                                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/10363427 Publication No. US20030195338A1
                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial
FEATURE:
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                                                                                                                                                INVENTION: Concatametric Immunoadhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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; ORGANISM: Homo sapiens US-10-363-427-18

Query Match 47.5%;
Best Local Similarity 64.5%;
Matches 272; Conservative 2:

22;

Score 1282.5; DB 14; Pred. No. 8.3e-78; 2; Mismatches 63; I

Indels

Gaps

11;

Length

617; 65;

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APPLICANT: LEE, Hye Ja
APPLICANT: CHOI, Eun Yong
APPLICANT: KIM, Jin Mi
APPLICANT: YIM, Soo Bin
TITLE OF INVENTION: Concatametric Immunoadhesion
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/363,427
CURRENT FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 52
SOFTWARE: KopatentIn 1.71
SEQ ID NO 22
LENGTH: 617
TYPE: PAT
ORGANISM: Homo sapiens
US-10-363-427-22
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US-10-363-427-22
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                                                                                                                                                                                                                             Query Match 47.5%; Score 1282.5; DB 14; Length 617; Best Local Similarity 64.5%; Pred. No. 8.3e-78; Matches 272; Conservative 22; Mismatches 63; Indels 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MeDexGen Inc.
APPLICANT: CHUNG, Yong Hoon
APPLICANT: HAN, Ji Woong
APPLICANT: LEE, Hye Ja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWT-----CTVLQNQKKVE 194
                                                                       273 KİKHLKTDDQDİYKVSIYDTKGKNVLEKIFDLK-----IQERVSKPKISWTCINTTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               615 PG 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     555 GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   495 NKALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 CEVMNGTDPELNL-----YQDGKHLKLSQRVI--THKWTTSLSAKFKCTA-GNKVSKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWT-----CTVLQNQKKVE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 KIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLK-----IQERVSKPKISWTCINTTLT
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326 CEVMNGTDPELNL-----YQDGKHLKLSQRVI--THKWTTSLSAKFKCTA-GNKVSKE 375
                                                                                                                                                     235 DDIKWEKTSDKKKIAQFRKEKE-----TFKEKDTYKLFK-----NGTL
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                                                                                                             95 IIKNLKIEDSDTYICEVEDOK-EEVOLLVFGLTANSDTHLLQGQ------SLTLT 142
                                                                                                                                                                                         35 DTVELTCTASOKKSIOFHWKNSNOIKILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPL
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2y 143 LESPPGSSPSVQCRSPRGKXIQGGKTLSVS	음 성
597 KDTSKNQVSLKLNSLTAADTAVYYCARNDRYAMDYWGQGTLVT 6	밁
<pre>2y 87WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT 142</pre>	S
Db 537 LVKPSETLSLTCTVSGFSLTNYGVHWVRQSPGKGLEWIGVKWSGGSTEYNAAFISRLTIS 596	밁
30 [S
Query Match 47.5%; Score 1282.5; DB 15; Length 972; Best Local Similarity 59.8%; Pred. No. 1.5e-77; Matches 274; Conservative 25; Mismatches 80; Indels 79; Gaps 10;	
S-1	
ORGAN FEATU	
SEQ ID N	
SOFTW	- .
PRIOR APPLICATION N PRIOR FILING DATE:	
PRIOR APPLICATION NUMBER: US 60/452, PRIOR FILING DATE: 2003-03-04	
PRIO	·. ·.
PRIOR APPLICATION NUMBER: US 60/3/3, PRIOR FILING DATE: 2002-04-18	·· ··
CURRENT APPLICATION NUMBER: US/10/418 CURRENT FILING DATE: 2003-04-17	
FILE REFERENCE: GC741-2	٠. ٠.
TITLE OF INVENTION: Production of	, -
APPLICANT	-
INFORMATIO	٠. ٠.
ESULT 15 S-10-418- Sequence Publicat	RE US
b 615 pg 616	р
y 430 PG 431	S
555 GOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 614	밁
370	Ş
495 NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGPYPSDIAVEWESN 554	Дb
310	δ
)b 435 DVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVCHQDWLNGKEYKCKVS 494	밁
250	Ş
376 SSVEPVSCPA-EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV 434	문
195	Ş

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APPLICANT: Power, Scott D.

APPLICANT: Wang, Huaming
APPLICANT: Ward, Michael
TITLE OF INVENTION: Production of Functional Antibodies in
TITLE OF INVENTION: Filamentous Fungi
FILE REFERENCE: GC741-2
CURRENT APPLICATION NUMBER: US/10/418,836
CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: US 60/373,889
PRIOR APPLICATION NUMBER: US 60/41,540
PRIOR APPLICATION NUMBER: US 60/41,540
PRIOR APPLICATION NUMBER: US 60/41,540
PRIOR APPLICATION NUMBER: US 60/452,134
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US-10-418-836-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: fusion protein US-10-418-836-39
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SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 39
LENGTH: 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 39, Application US/10418836 Publication No. US20040018573A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 47.5%; Score 1282.5; DB 15; Length 975;
Similarity 59.8%; Pred. No. 1.5e-77;
74; Conservative 25; Mismatches 80; Indels 79;
TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                                                                                                                                                                                                                                     --WDQGNFPLIIKNLKIEDSDTYIÇEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTLT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                   QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPP
                                                                                                                                                                                                                                                       VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
                                                                                                                                                                                                                                                                                                         LESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS------QLEL
                                                                                                                                                                                                                                                                                                                                                           KDTSKNQVSLKLNSLTAADTAVYYC------ARNDRYAMDYWGQGTLVT
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                                                 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                              ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                     QDSG-----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC--
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GENERAL INFORMATION:
APPLICANT: HOTWITZ, Arnold H.
APPLICANT: HOTWITZ, Arnold H.
TITLE OF INVENTION: Methods and Materials Fo
FILE REFERENCE: 13598US01
CURRENT APPLICATION NUMBER: US/10/404,724
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/368,530
PRIOR FILING DATE: 2002-03-29
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin version 3.2
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US-10-404-724-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23, Application US/10404724 Publication No. US20030203447A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo
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                                   393
420 HYTQKSLSLSPG 431
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                                                                                                                                                                                                                                                                 219 NV--NHKPSNTKVD----KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS
                                                                                                                                                                                                                                                                                     185 TVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMIS
                                                                                                                                                                                                                                                                                                                                         159 ALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYIC
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                                     SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
                                                           SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
                                                                                                           NGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYP
                                                                                                                                NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
                                                                                                                                                                                      RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
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HYTQKSLSLSPG

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RESULT 19
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; ORGANISM: Homo sapiens
US-10-656-769-32
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US-10-656-769-32
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CURRENT FILING DATE: 2003-09-05
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin version 3.0
SEQ ID NO 32
LENGTH: 467
Sequence 3, Application US/09747669
Patent No. US20020122807A1
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
APPLICANT: Saleh, Mansoor
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
TITLE OF INVENTION: 4B5 THAT SPECIFICALLY DETECT CANCER C
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Best Local Similarity
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APPLICANT: Qian, Xueming
TITLE OF INVENTION: Therapeutic Human Anti-IL-IR
FILE REFERENCE: 01,1554
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APPLICANT: Witte, Alison
APPLICANT: Vezina, Chris
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Pred. No. 8.6e-78;
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     NUCLEOTIDES
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US-10-290-703-3

GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

APPLICANT: Saleh, Mansoor

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED

TITLE OF INVENTION: 485, THAT SPECIFICALLY DETECT CANCER

TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THERE

TITLE OF INVENTION: AND DETECTION OF CANCERS

FILE REFERENCE: 316082001002

CURRENT APPLICATION NUMBER: US/10/290,703

CURRENT FILING DATE: 2002-11-08

PRIOR APPLICATION NUMBER: US 09/747,669

INCER CELLS,

NUCLEOTIDES
THE PROPHYLAXIS

Sequence 3, Application US/10290703 Publication No. US20030118593A1

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RESULT 20
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CURRENT APPLICATION NUMBER: US/09/747,669
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 09/111,286
PRIOR APPLICATION NUMBER: US 09/111,286
PRIOR FILING DATE: 1998-07-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches
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ORGANISM: Artificial
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nes 280; Conserv
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                                              HYTOKSLSLSPG
                                                                                                                                 SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
                                                                                                                                                                          NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
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                                                                             HYTOKSLSLSPG 431
                                                                                                             SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
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Pred. No. 8.8e
27; Mismatches
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8.8e-78;
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PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: US 09/111,286
PRIOR FILING DATE: 1998-07-07.
PRIOR APPLICATION NUMBER: US 60/051,945
PRIOR FILING DATE: 1997-07-08
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 3
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US-10-378-567-2
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Publication No. US20040006208A1
GENERAL INFORMATION:
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Best Local (
APPLICANT: KARPUSAS, MICHAEL
APPLICANT: HSU, YEN-MING
APPLICANT: TAYLOR, FREDERICK R.
APPLICANT: ZHENG, ZHONGLI
TITLE OF INVENTION: CO-CRYSTAL STRUCTURE OF MONOCLONAL ANTIBODY SCE
TITLE OF INVENTION: CD154, AND USE THEREOF IN DRUG DESIGN
FILE REFERENCE: A096CON1
CURRENT APPLICATION NUMBER: US/10/378,567
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: PCT/US01/27352
PRIOR TING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 60/276,452
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ORGANISM: Artificial
FEATURE:
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Local Similarity 56.9%; Pred. No. 8.8e-78;
hes 280; Conservative 27; Mismatches 91
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RESULT 22
US-10-207-655-344
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; OTHER INFORMATION: US-10-207-655-344
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Best Local Sim
Matches 275;
                                                                              APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 344
LENGTH: 492
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PRIOR APPLICATION NUMBER: 60/229,933
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                     Sequence 344, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
                                                                   LENGTH: 49
                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 448
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                             401
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75; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
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               fusion
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               polypeptide
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Pred. No. 8.8e-7
1; Mismatches
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74; I
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Query Match

Score 1279;

DB

14;

Length 492;

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RESULT 23
US-10-108-260A-4292
Sequence 4292, Application US/10108260A
PUBLICATION WO. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US20040005560A1e1 full length cDN.
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4292
LENGTH: 470
TYPE: PAT
ORGANISM: Homo sapiens
US-10-108-260A-4292
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Best Local Similarity
Matches 281; Conserv
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121 HEVRALFD-HWGQGTLVTVSSASTKG--PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 177
                                 123 FGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTL 169
                                                                                75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 -----VEDQK-------EEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSP 151
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                                                                                                                                                                                                15 QLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKN------SNQIKIL 62
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                                                                            G-RPNYAQKFQDRVTISADESSSI-----VYMDLDRLTIEDTAIYFCAI------LLE 120
                                                                                                                                                        QVQLVQSGTE----VKKPGSSVKVSCKASGGSFSSVVFTWVRQAPGEGLEWMGSIIPIL
                                                                                                                   GNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
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232 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYYDGVEVHNAKTKPREEQYNSTYRVVSVL 291 	8 & &	
182 WTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPK 231	Qy Db	
152 SVQ-CRSPRGKNIQGGKT	Qy Db	
111VEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPEGSSP 151	Db Qq	
ILGNQGSFLTKGPSKLNDRADSRRSLMDQG-NFPLIIKNLKIEDSDTYICE		
1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60	₽ 2	
'Match 47.3%; Score 1277; DB 14; Length 543; Local Similarity 55.8%; Pred. No. 1.7e-77; Les 279; Conservative 33; Mismatches 92; Indels 96; Gaps 13	Query Ma Best Loc Matches	
ESULT 24 S-10-207-655-345 Sequence 345, Application US/10207655 Sequence 345, Application US/10207655 Sequence 345, Application US20030118592A1 GENERAL INFORMATION: APPLICANT: Ledbetter, Jeffrey A. APPLICANT: Hayden-Ledbetter, Martha S. APPLICANT: Hayden-Ledbetter, Martha S. APPLICANT: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS FILE REFERENCE: 390069 401C1 CURRENT APPLICATION NUMBER: US/10/207,655 CURRENT FILING DATE: 2002-07-25 NUMBER OF SEQ ID NOS: 426 SOFTWARE: Patentin version 3.0 SEQ ID NO 345 LENGTH: 543 TYPE: PRT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: fusion polypeptide	RESULT 24 US-10-207-655- Sequence 345 Sequence 345 Publication GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT FILE OF IN- CURRENT APP CURRENT APP CURRENT APP CURRENT OF S SOFTWARE: P SEQ ID NO 34 LENGTH: 54 TYPE: PRT ORGANISM: FEATURE: CHER INFO US-10-207-655-	
412 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 469	Db	
374 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431	Ş	
352 PAPIEKTISKAKGQPREPQVYALPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 411	DЪ	
314 PAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPE 37	γQ	
9 (D 45	
EDDEVKENMYVDGVEVHNAKTKPREEOYNSTYRVSVI.TVI.HODMI.NGKEYKCKVSNKAI.	₹ ¦	
199 IVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH 253 	B 8	
178 TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD 235	В	
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APPLICANT: MORROW, PHILLIP

APPLICANT: MORROW, PHILLIP

TITLE OF INVENTION: NECTIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR

TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR

TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF

FILE REFERENCE: 037003-0275759

CURRENT APPLICATION NUMBER: US/09/740,002

CURRENT APPLICATION NUMBER: 09/335,697

PRIOR APPLICATION NUMBER: 09/335,697

PRIOR APPLICATION NUMBER: 09/335,697

PRIOR APPLICATION NUMBER: 09/335,697

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PRIOR APPLICATION NUMBER: 08/488,376

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-002-25
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US-09-740-002-25
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y Match 47.2%; Score 1276.5; DB 9; Length Local Similarity 57.1%; Pred. No. 1.5e-77; hes 281; Conservative 27; Mismatches 87; Indels
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                                                                                                                                                                                                  NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
HYTQKSLSLSPG
                                                                                   SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
                                                                                                                                                                                                                                                                                RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQEWL
                                                                                                                                                                                                                                                                                                                 RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
                                                                                                                                                                                                                                                                                                                                                                                              NV--NHKPSNTKVD----KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMIS
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                                                                                                                                                                       NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYP
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                                                  SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
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CURRENT APPLICATION NUMBER: US/10/325,698
CURRENT FILLING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US/09/740,002
PRIOR FILLING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR FILLING DATE: 1999-06-18
PRIOR FILLING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR FILLING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN Ver: 2.1
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Matches
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LENGTH: 475
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APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTI-
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
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463
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HYTOKSLSLSPG
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                                                                       SDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
                                                                                                    SDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
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CURRENT APPLICATION NUMBER: US/10/138,727A
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.0
SEQ ID NO 41
LENGTH: 579
TYPE: PRT
ORGANISM: Artificial sequence
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                                                                                                                                          RESULT 28
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Publication No. US20040131591A1
GENERAL INFORMATION;
APPLICANT: Oxfard Biomedica (UK) Ltd.
APPLICANT: Kingsman, Alan
APPLICANT: Bebbington, Christopher
APPLICANT: Carroll, Miles
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Best Local Similarity
Matches 281; Conserv
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RESULT 29
US-10-320-231A-79
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APPLICANT: Myers, Kevin
APPLICANT: Lamikandra, Abigail
TITLE OF INVENTION: VECTOR SYSTEM
FILE REFERENCE: 53268200920
CURRENT APPLICATION NUMBER: US/10/334,235
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 10/060,585
PRIOR FILING DATE: 2002-01-29
PRIOR FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: DCT/GB00/04317
PRIOR APPLICATION NUMBER: US 09/445,375
PRIOR APPLICATION NUMBER: US 09/445,375
PRIOR FILING DATE: 1998-06-04
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Best Local Similarity
Matches 277; Conserv
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 38
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                         DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                           GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                                                       GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                                                                                                                                                                                                              DKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKP----
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                                                                               DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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ilarity 59.4%;
Conservative 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16;
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172

314

256

134

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; Sequence 79, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Ce
; TITLE OF INVENTION: Treatment Of Asthma
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A

Cell Factor Activity

And Use

For

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RESULT 30
US-10-150-475A-6
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; OTHER INFORMATION: synthetic sequence
US-10-320-231A-79
                                                                    SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 6
LENGTH: 444
TYPE: PRT
                                                                                                                                                                                                                                                                                   Sequence 6, Application US/10150475A Publication No. US20030103985A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US 60/342,174
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin version 3.2
SEQ ID NO 79
SEQ ID NO 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/150,475A CURRENT FILING DATE: 2002-05-17 PRIOR APPLICATION NUMBER: US 60/307,451 PRIOR FILING DATE: 2001-07-24 NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                               APPLICANT: Adolf, G. et al.
TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
FILE REFERENCE: 1/1211
OTHER INFORMATION: Description of Artificial Sequence: Humanised OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO:
                                 ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RFTIS-RDNSKNTLYLOMN-----SLRAEDTAVYYCARRD-----FFAHFD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGKKGDTVELTCTAS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
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Pred. No. 1.9e-77
Pred. No. 1.9e-77
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TITLE OF INVENTION: Compositions and methods for TITLE OF INVENTION: cytotoxic CD44 Antibody Imm FILE REFERENCE: 1/1414

CURRENT APPLICATION NUMBER: US/10/704,522

CURRENT FILING DATE: 2003-11-07

PRIOR APPLICATION NUMBER: US 60/429,516

PRIOR APPLICATION NUMBER: US 60/429,516

PRIOR APPLICATION NUMBER: EP 02024881

PRIOR APPLICATION NUMBER: EP 02024881

PRIOR FILING DATE: 2002-11-08

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 6

LENGTH: 444

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

FEATURE:
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US-10-704-522-6
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                                                                                                                                                                                     ; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain US-10-704-522-6
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APPLICANT: Adolf, Gunther
APPLICANT: Baumann, Michael
APPLICANT: Heider, Karl-Heinz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10704522
Publication No. US20040120949A1
                                                                                                              Matches
                                                                                                                             Query Match
Best Local S
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Best Local :
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 77
                                  11 LVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYYLDSIKGRFTI 70
                                                                       30 LGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKILGNQGSFL----TKGPSKL
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                                                                                                            Similarity 59.: 75; Conservative
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NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
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                                                                                                                             47.1%;
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                                                                                                            27;
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Pred. No. 2.2e-
27; Mismatches
                                                                                                          Score 1273.5; DB
Pred. No. 2.2e-77;
7; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2e-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for treating cancer using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoconjugates
                                                                                                                                                 DB 16;
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                                                                                                          Indels
                                                                                                                                             Length 444;
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FILE REFERENCE: 1/1383
CURRENT APPLICATION NUMBER: US/10/645,215
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: ED 02 018 686.2
PRIOR FILING DATE: August 21, 2002
PRIOR APPLICATION NUMBER: US 60/405,956
PRIOR FILING DATE: August 26, 2002
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
LENGTH: 444
TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Adolf, Guenther
APPLICANT: Baum, Anke
APPLICANT: Heider, Karl-Heinz
APPLICANT: Heider, Karl-Heinz
APPLICANT: Compositions and Methods for Treating Cancer using
TITLE OF INVENTION: Cyclocxic CD44 Antibody Immunoconjugates and
TITLE OF INVENTION: Chemotherapeutic Agents
                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 275; Conserv
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                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                      11: LVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYYLDSIKGRFTI
                                                                                                  TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK 219
                                                                                                                                  NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG
                                                                                                                                                                                                        LGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKILGNQGSFL-----TKGPSKL
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                                                                  QSLTLTLESPPGSSPSVQCRSPRGKNIQGG------
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 --QLELQDSG---
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                          47.18;
59.38;
                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                          Score 1273.5; DB 16; Pred. No. 2.2e-77;
                                                                                                                                                                                                                                          Mismatches
 ----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                                                                                                                                                                                                                                          69;
                                                                    ----KTLSVS----
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RESULT 33
US-09-740-002-27
; Sequence 27, Application US/09740002
; Patent No. US20020001798A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 276; Conserv
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES TITLE OF INVENTION: SPECIFIC TO RSV F-ROTEIN AND METHODS FOR THEIR TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF FILE REFERENCE: 037003-0275759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BRAMS, PI
APPLICANT: MORROW,
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VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 308
                                                                                       EFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVPLFPPKFKDTLMISRTPEVTCVV
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                                                                                                                                                                                                                                                  VQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------ 166
                                                                                                                                                                                                                                                                                                                                                          LVAVATRVLSQVQLQESGPALVKPTQTLTLTCTFSGFSLSTRGMSVNWIRQPPGKALEWL
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                                                                                                                                          FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPS
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                                                                                                                                                                                                                                                                                                                        ----GNQGSFLTKG-PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEE 117
                                                                                                                                                                                                                                                                                                                                                                                                                            47.1%; Score 1273.5; DB ilarity 57.1%; Pred. No. 2.4e-77; Conservative 29; Mismatches 99
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APPLICANT: MORROW, PHILLIP

APPLICANT: MORROW, PHILLIP

TITLE OF INVENTION: NETER

TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR

TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF

FILE REFERENCE: 037003-0275759

CURRENT APPLICATION NUMBER: US/10/325,698

CURRENT APPLICATION NUMBER: US/09/740,002

PRIOR APPLICATION NUMBER: US/09/740,002

PRIOR FILING DATE: 2000-12-20

PRIOR FILING DATE: 2000-12-20

PRIOR FILING DATE: 0000-12-20

PRIOR APPLICATION NUMBER: 09/335,697

PRIOR FILING DATE: 1999-06-18

PRIOR FILING DATE: 1999-06-18

PRIOR FILING DATE: 1999-06-07

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 27

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US-10-325-698-27
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US-10-325-698-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27, Application US/10325698 Publication No. US20040076631A1 GENERAL INFORMATION:
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                                                                                                                                            VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
                                                                                                                                                                                                 NTKVD----KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                                                                                                                                                                                                                                                                            FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPS
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NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
                                                               SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES
                                                                                                                   VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
                                                                                                                                                                                                                                       EFKIDIVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                                                                                                                                                                                                                                                                                                                   --KTLSVS------QLELQDSG------TWTCTVLQNQKKV 193
                                                                                                                                                                                                                                                                                                                                                                                               VQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------
                                                                                                                                                                                                                                                                                                                                                                                                                                         ARIDWDDDTFYSASLKTRLSISKDTSKN-----QVVLRMTNVDPVDTATYFCARASLYDS
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                                       SNKALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWES
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APPLICANT: KAVANAUGH, William M.
APPLICANT: Ballinger, Marcus
ITILE OF INVENTION: FIBROBLAST GROWTH FACTOR
ITILE OF INVENTION: FIBROBLAST GROWTH FACTOR
ITILE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUS
FILE REFERENCE: PP01474.101
CURRENT APPLICATION NUMBER: US/10/683,255
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: 09/499,846
PRIOR FILING DATE: 2000-02-07
PRIOR APPLICATION NUMBER: 60/119,002
PRIOR PILING DATE: 1999-02-08
NUMBER OF SEQ ID NOS: 12
SOCTWARRE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 497
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US-10-683-255-6
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Publication No. US20040063910A1
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Best Local
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                    123 FGLTANSDTHLLQGQSLTLTLESPP------GSS-----PSVQCRSPRGKNI 163
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                                                                                                                                                                           SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
                                                                                                                                                                                                                   EGSGSPGLQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                    ----APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
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PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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57.5%;
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Pred. No. 2.5e
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US-10-683-255-4
; Sequence 4, Application US/10683255
; Publication No. US20040063910A1

RESULT 36

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CURRENT APPLICATION NUMBER: US/10/683,255
; CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: 09/499,846
PRIOR APPLICATION NUMBER: 09/499,846
PRIOR APPLICATION NUMBER: 60/119,002
PRIOR TILING DATE: 1999-02-08
NUMBER OF SEQ ID NOS: 12
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapiens
US-10-683-255-4
Sequence 2, Application US/10683255
PUBLICATION NO. US20040063910A1
GENERAL INFORMATION:
APPLICANT: KAVANAUGH, William M.
APPLICANT: Ballinger, Marcus
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUS
FILE REFERENCE: PP01474 101
CURRENT APPLICATION NUMBER: US/10/683,255
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: 60/419,846
PRIOR APPLICATION NUMBER: 60/119,002
PRIOR APPLICATION NUMBER: 60/119,002
PRIOR APPLICATION NUMBER: 60/119,002
PRIOR APPLICATION NUMBER: 60/119,002
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US-10-683-255-2
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APPLICANT: Ballinger, Marcus
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN
FILE REFERENCE: PP01474.101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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                                                                                                                                                                                  FUSION
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APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US20040005560Alel ful
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4282
LENGTH: 474
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                                                                                                          ; TYPE: PRT
; ORGANISM: Homo
US-10-108-260A-4282
                                                                                                                                                                                                                                                                                                                                         RESULT 38
US-10-108-260A-4282
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                                                 Best Loc
Matches
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                         Sequence 4282, Application US/10108260A
Publication No. US20040005560A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 47.1%;
Best Local Similarity 57.0%;
Matches 276; Conservative 3
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                                                                            Query Match
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ORGANISM: Homo
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                                                 280;
16 LALLPAATQGNKVV-----LGKKGDTVELTCTASQKKSIQF-----HKNSNQIKILGNQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 QLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW-KNSNQIKILGNQGSFLTKGP
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                                                            47.1%;
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                                               Score 1272.5;
Pred. No. 2.8e
28; Mismatches
                                                            5; DB 15;
1.8e-77;
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                                               84; Indels
                                                                            Length
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RESULT 39
US-10-660-128-12
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                                                                                                                                                                                                        PRIOR FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: US 60/072,481
PRIOR FILING DATE: 1998-01-26
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 12
LENGTH: 476
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/10660128 Publication No. US20040120947A1 GENERAL INFORMATION:
Best Local Similarity
Matches 273; Conserv
                   Query Match
Best Local
                                                                   FEATURE:
NAME/KEY: Misc feature
LOCATION: 20
OTHER INFORMATION: Xaa may be glutamine or glutamic
-10-660-128-12
                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/09/584,166
PRIOR TILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 09/32,875
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: US 09/237,299
PRIOR TILING DATE: 1999-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kim, Kyung Jin
TITLE OF INVENTION: DR4 Antibodies and Uses
FILE REFERENCE: P1245R1P2B
                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/660,128
CURRENT FILING DATE: 2003-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ashkenazi, Avi APPLICANT: Chuntharapai,
                                                                                                                                                      OTHER INFORMATION: Sequence is synthesized
                                                                                                                                                                          FEATURE:
                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           407
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Dodge, Kelly
   Conservative
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               47.1%; Score 1272; DB 16; 60.4%; Pred. No. 3e-77;
   29;
   Mismatches
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   82;
                                   Length 476;
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                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-159-006-18
                                                                                                                                                                                                                                            SEQ ID NO 18
LENGTH: 453
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Garin-Chesa,
APPLICANT: Bamberger, U
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                                                                                                                                        Matches
                                                                                                                                                        Query Match
Best Local
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/159,006
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 99/301,593
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: EP 98107925.4
PRIOR FILING DATE: 1998-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FAPa-specific Antibody with Improved Producibility
FILS REFERENCE: 0652.1890002
                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Vei
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/086,049 PRIOR FILING DATE: 1998-05-18
                                                                                                                                      271;
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70
                              87 W----DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ---GQSLTL 141
                                                                   10
                                                                                                   30 LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQGSF-LTKGPSKLNDRADSRRSL
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                                                                                                                                                        Similarity
TVGKSSSTAYMELRSLTSEDSAVYFC---
                                                                 LVKPGASVKMSCKTSRYTFTEYTIHWVRQSHGKSLEWIGGINPNNGIPNYNQKFKGRATL
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Bamberger, Uwe
Leger, Olivier
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10. US20030143229A1
                                                                                                                                    47.1%; ilarity 59.0%; Conservative 3
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                                                                                                                                                                                                                                                                                    : 108
2.0
                                                                                                                                    31;
                                                                                                                                                      Score 1271.5;
Pred. No. 3.1e
                                                                                                                                        Mismatches
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-- ARRRIAYGY---DEGHAMDYWGQGTSV
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                                                                                                                                        84; Indels
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CURRENT APPLICATION NUMBER: US/10/404,724
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/368,530
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-404-724-25
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US-10-404-724-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Horwitz, Arnold H.
TITLE OF INVENTION: Methods and Materials
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 13698USO
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                                                                                                                                                                                                                                                                                                                                                                                                                 11 LLVLQLALLPAATQGNKVVLG----KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQG
                                                                                                                                                                                                                                                                                                64 LEWMGWINTYTEEPTYGQKF-------QGRFTFTLDTSTSTAYLEISSLRSEDTA 111
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MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
                                                              YICNV--NHKPSNTKVD----KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL
                                                                                                  WTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPKPKDTL
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                                                                                                                                       GTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT
                                                                                                                                                                                                                                                                                                                                                                           LLFLMAAAQSAQAQIQLVQSGAEVKKPGESVKISCKAS---GYTFTKYGMNWVRQAPGQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
                                                                                                                                                                                                                                                                                                                                    -----SFLTKGPS---KLNDRADSRRSLWDQGNFP------LIIKNLKIEDSD 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.1%;
                                                                                                                                                                               ----KTLSVS----
                                                                                                                                                                                                                     ----ARFGSAVD-----YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1271.5; DB Pred. No. 3.2e-77;
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US-10-207-655-15
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CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 15
LENGTH: 499
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/10207655 Publication No. US20030118592A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN
FILE REFERENCE: 390069.401C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: DOMAIN
LOCATION: (266)..(499)
OTHER INFORMATION: HUMAN IGG1 WILD TYPE HINGE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SITE LOCATION: (1).
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      306
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                                                                                                                                                                                                                                                                                                                126 --- TANSDTHLLQ-GOSLTLTLESPPGSSPSVQCR------SPR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              275;
                                                                                                                                                                                                                                                                                                                                                          82
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    CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE 365
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                                          CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
                                                              CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 305
                                                                                                                    FDVWGTGTTVTVSDQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
                                                                                                                                                                                                 GAIYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWY
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                                                                                                                                           IDI------VPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVT 245
                                                                                                                                                                                                                                                                              SGGGGSSQAYLQQSGAELV-----RPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                   SQSPAILSASPGEKVTMTCRASSSVS-YMHWYQQKP----GSSPKPWIYAPSNLASGVPA
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56.6%;
                                                                                                                                                                                                                                       GKNIQGGKTLSV------SQLELQDSGTWTCTVLQNQKKVEFK 196
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RESULT 43
US-10-207-655-148
; Sequence 148, Application US/10207655
; Publication No. US20030118592A1
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Best Local Similarity
Matches 275; Conserv
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APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 148
LENGTH: 499
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ORGANISM: Artificial Sequence
FEATURE:
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                          LSLSPG 431
                                                                   WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
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                                                                                                                                                                CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 372
                                                                                                                                                                                 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
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LSLSPG
                                                     WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
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Pred. No. 3.5
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es 93; Indels 91;
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Sequence 15, Application US/10053530

Publication No. US200301339381

GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey
APPLICANT: Hayden-Ledbetter, Martha
TITLE OF INVENTION: Binding Domain-Immunoglobulin Fusion Pro
FILE REFERENCE: 390069.401

CURRENT APPLICATION NUMBER: US/10/053,530

CURRENT FILING DATE: 2002-01-17

PRIOR APPLICATION NUMBER: US 09/765,208

PRIOR APPLICATION NUMBER: US 09/765,208

PRIOR FILING DATE: 2001-01-17

NUMBER OF SEQ ID NOS: 38

SOFTWARE: Patentin version 3.0

SEQ ID NO 15
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US-10-053-530-15
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LOCATION: (266)..(499)
OTHER INFORMATION: HUMAN IGG1 WILD TYPE HINGE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: MOUSE-HUMAN HYBRID FUSION NAME/KEY: SITE LOCATION: (1)..(265)
OTHER INFORMATION: MOUSE ANTI-HUMAN CD20 SCFV
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ORGANISM: Artificial Sequence
FEATURE:
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                                 426 LSLSPG
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                                                                         WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
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LSLSPG
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                                 431
498
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RESULT 45 US-09-948-429B-12

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TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acids
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Patent No. US20020177689A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OS B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: THERMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 47.0%; Score 1271; DB 9; Length 476; Best Local Similarity 59.8%; Pred. No. 3.5e-77; Matches 274; Conservative 29; Mismatches 87; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Teskin, Robin L.
REGISTRATION NUMBER: 310
REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: US 08/487,550
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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CITY: Alexandria
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CLASSIFICATION:
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ZIP: 22314
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258
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                                                                                                                                                                                                                                                                144 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 203
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                                                                                       CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                   QDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC--
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177 ODGGTWTCTVTONOKKVERKTDIVDODADARKGCDKTHTC 216	143 LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLEL 176	86 LWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT 142 :	30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRS 85	Query Match 47.0%; Score 1271; DB 12; Length 476; Best Local Similarity 59.8%; Pred. No. 3.5e-77; Matches 274; Conservative 29; Mismatches 87; Indels 68; Gaps 11;	RESULT 46 US-09-758-173-12 US-09-758-173-12 Sequence 12, Application US/09758173 Publication No. US20010024648A1 PUBLICATION NO. US20010024648A1 FITTLE OF INVENTION: "MONEEY MONOCIONAL ANTIBODIES SPECIFIC TITLE OF INVENTION: "MONMER OF 1 ANTIBODIES SPECIFIC TITLE OF INVENTION: TO HUMAN BT 1 AND/OR BT 2 PRIMATIZED FORMS TITLE OF INVENTION: TO HUMAN BT 1 AND/OR BT 2 PRIMATIZED FORMS TITLE OF INVENTION: TO HUMAN BT 1 AND/OR BT 2 PRIMATIZED FORMS TITLE OF INVENTION: TO HUMAN BT 1 AND ORDERS THEREOF, TITLE OF INVENTION: TO HUMAN BT 1 AND ORDERS THEREOF AS TITLE OF INVENTION: TO HUMAN BT 1 AND ORDERS THEREOF AS TITLE OF INVENTION: INVONSUPRESANTS NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS: ADDRESSEE: BURKS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Alexandria STREET: 499 Prince Street CITY: Alexandria TYPE: PADALE FORM: COMPUTER EADDRESS: 1005/MS-DOS SOFTWARE: VA COUNTRY: USA COUNTRY: USA COMPUTER EADDRESS: 005/MS-DOS SOFTWARE: PACE COMPATIBLE ORDERS COMPUTER: APPLICATION NUMBER: US/09/756,173 FILING DATE: OF-UN-1956 CORRESPONDENCE OF TOWN DATA: APPLICATION NUMBER: US/09/756,173 FILING DATE: OF-UN-1956 FILING DATE: US 08/487,550 FILING DATE: US 08/487,550 REFERENCE/DOCKT UNMER: 03/383,916 FILING DATE: OF-UN-1956 FILING DAT	394 KLTYDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431 	378 YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLXS 437

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US-10-124-905-12
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                                               Query Match
Best Local Sim
Matches 274;
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                                                                                                                                                                                                    TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CONTRIBUT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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ADDRESSEE: BURNS, DO
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                                                                                                                                                                                                                                                              NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01
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30 LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRS
                                                             Similarity
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                                            47.0%; Score 1271; DB 13; ilarity 59.8%; Pred. No. 3.5e-77; Conservative 29; Mismatches 87;
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                                                                          Length 476;
                                             Indels
                                               68;
                                               Gaps
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US-10-124-807-12
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           TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01:
                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 703-836-6620
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LENGTH: 476 amino acids
                               TELEPHONE: 703-021
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THEREOF

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258 CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
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KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 475
                                  KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                          YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                                                                                        TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
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                                                                                                             YTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISTDTSKNOFSLKLNSMTAADTAVYYC-VRDRLFSVVGMVY----NNWFDVWGPGVLVT
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Sequence 12, Application US/10124807
Publication No. US20030166207A1
GENERAL INFORMATION: COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/124,80 APPLICATION NUMBER: US 08/487,550 FILING DATE: 07-JUN-1995 BURNS, DOANE, SWECKER & MATHIS , Darrell R.
"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THER IMMUNOSUPPRESANTS" 09/383,916 US/10/124,807 012712-131 Version #1.30

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TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
FILE REFERENCE: 037003/291872
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US/10/291,532
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: 09/758,173
PRIOR APPLICATION NUMBER: 09/758,173
PRIOR APPLICATION NUMBER: 09/758,173
PRIOR APPLICATION NUMBER: 09/758,173
PRIOR APPLICATION NUMBER: 09/383,916
PRIOR APPLICATION NUMBER: 09/383,916
PRIOR APPLICATION NUMBER: 08/487,950
PRIOR APPLICATION NUMBER: 08/487,950
PRIOR APPLICATION NUMBER: 08/487,950
PRIOR APPLICATION NUMBER: 08/487,950
PRIOR FILING DATE: 1999-08-66-07
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: primatized peptide sequence US-10-291-532-12
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US-10-291-532-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: HARIHARAN, KANDASAMY
APPLICANT: HANNA, NABIL
                                                                                                                                          NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. :
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/10291532 Publication No. US20030180290A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                             FEATURE:
                                                                                                                       LENGTH: 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   378
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US-10-207-655-348
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 348
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Publication No. US20030118592A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 274; Conservat
                                                                                                                                                                                     Matches
                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                      LENGTH: 504
                                                                                                                                                                                     282;
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                                                  66 TVKLL----IYYT---SRLHSGVPSRFSGSGSGTDYSLTIANLQPEDIATYFCQ-----
EVQLLVFGLTANSDTHLLQGQSL----
                                                                                                                                                  MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW----KNSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----QLEL
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                                                                                QIKILGNQGSFLTKGPSKLNDRADSRRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKE 116
                                                                                                                   MSRGVDIQ------MTQTTSSLSASLGDRVTISCRASQDIRNYLNWYQQKPDG
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                                                                                                                                                                                  47.0%; ilarity 55.0%; Conservative 29
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                                                                                                                                                                                  ; Score 1271; DB 14
; Pred. No. 3.8e-77;
29; Mismatches 92
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                                                                                                                                                                                                                     DB 14;
                 -----PGSSPSV 153
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                                                                                                                                                                                                                     Length 504;
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APPLICANT: HELIX RESEARCH INSTITUTE

ITITLE OF INVENTION: NO. US20040005560Alel full length cDN.

FILE REFERENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/10/108,260A

CURRENT FILING DATE: 2002-03-27

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4278

LENGTH: 473

TYPE: PAT

ORGANISM: Homo sapiens

US-10-108-260A-4278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-108-260A-4278
US-10-108-260A-4278
; Sequence 4278, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                      13 VLQLALLPAA-TQGNKVVLG----KKGDTVELTCTAS--QKKSIQFHW-----KNSNQI
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              VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 307
                                                                      VEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCV
                                                                                                         YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKP
                                                                                                                                                                                                                       AVISFDGTKKYYADSVKGRFTVSRDNSRNTLD-----LLMDGLRPEDTAVYSCAKAPFN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---LELQDSGTWTCTVLQNQKKVEFKID-----IVPCPAPEPKSCDKTHTC----
                                                                                                                                                                                                                                                  KILGNQGS---FLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE 116
                                                                                                                                                                                                                                                                              VFLVALLRGVHCQGQLVQSGGGVVQPGRSLRLSCEASGFSFKFFNMHWVRQAPGKGLEWV
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VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK
                                                      SNTKVD----KRVEPKSCDKTHTCPPCPAPELLGGPSVFLIPPKPKDTLMISRTPEVTCV
                                                                                                                                      ---KTLSVS-----TWTCTVLQNQKK 192
                                                                                                                                                                 ----LVRGVHGAFD---LWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD 174
                                                                                                                                                                                           EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------
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FILE REFERENCE: DOOGNE
CURRENT APPLICATION NUMBER: US/09/910,600
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/220,139
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 32
LENGTH: 619
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial
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US-09-910-600-32
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Best Local Similarity 57.8%;
Matches 273; Conservative 2
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APPLICANT: Chang, Han
APPLICANT: Whitney, Gena
TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
567
                    380 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                            TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
                                                                                                TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
                                                                                                                                                   PEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
                                                                                                                                                                                                                                                                                                            -RLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSV---HD
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Pred. No. 5.8e
27; Mismatches
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5.8e-77:
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APPLICANT: Andras Aszodi
APPLICANT: Jose W. Saldanha
APPLICANT: Bruce M. Hall
TITLE OF INVENTION: Therapeutic binding molecules
FILE REFERENCE: PCT/EP0Z/01420
CURRENT APPLICATION UNMBER: US/10/467,546
CURRENT FILING DATE: 2003-08-08
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 448
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US-10-467-546-4
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US-10-656-769-20
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FEATURE:
NAME/KEY: MISC_FEATURE
OTHER INFORMATION: Amino acid sequence of chimeric heavy chain
US-10-467-546-4
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Sequence 20, Application US/10656769
Publication No. US20040097712A1
GENERAL INFORMATION:
APPLICANT: Varnum, Brian
APPLICANT: Witte, Alison
APPLICANT: Witte, Alison
APPLICANT: Wong, Lu Min
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Publication No. US20040096901A1
GENERAL INFORMATION:
APPLICANT: Gregorio Aversa
APPLICANT: Frank Kolbinger
APPLICANT: Jose M. Carballido Herrera
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                           SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                     SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                        PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387
                                                                                                                                                                                                                                                                                                                                                                                EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKSCDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADSRRSLW----DOGNFPLIIKNLKIEDSDTYICEVEDOKEEVOLLVFGLTANSDTHLLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVKPGASVKMSCKASGYTFTNYIIHWVKQEPGQGLEWIGYFNPYNHG-----TKYNEK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                             THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----
                                                                                                                                                                                                                                                                                      PREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDG
                                                                                                                                                                                                                                                                                                                                                               EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                       THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKPNWYVDGV
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Pred. No. 4.1e-77;
7; Mismatches 73; Indels 89;
                                                                                                                                                                                                             447
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; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-656-769-20
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Matches
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CURRENT FILING DATE: 2003-09-05
NUMBER OF SEQ ID NOS: 79
SOFTWARE: Patentin version 3.0
SEQ ID NO 20
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody
FILE REFERENCE: 01,1554
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VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -FWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 186
                                                                                                                                                                                                                                                         AKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGVV---QPGRSLRLSCAASGFTFSNYGMHWVRQAPGKGLEWVAGIWNDGINKYHAHSVR 84
                                                                                                                                                                         AKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVL
                                                                                                                                                                                                                                                                                                                                                  VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
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APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560Alel full length cDNA;
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4073
LENGTH: 472
TYPE; PRT
ORGANISM: Homo sapiens
US-10-108-260A-4073
Query Match
Best Local Similarity 59.5%; Pred. No. 4.8e-77;
Best Local Similarity 59.5%; Pred. No. 4.8e-77;
Matches 275; Conservative 24; Mismatches 83; Indels 80; Gaps
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RESULT 55 US-10-108-260A-4073

Sequence 4073, Application US/10108260A Publication No. US20040005560A1 GENERAL INFORMATION:

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30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQ 89

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Sequence 4285, Application US/10108260A

Publication No. US20040005560A1

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1el full length cDNA
FILE REFERENCE: H1-A0106

CURRENT APPLICATION NUMBER: US/10/108,260A

CURRENT FILING DATE: 2002-03-27

NUMBER OF SEQ ID NOS: 5458

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4285

LENGTH: 471
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US-10-108-260A-4285
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                                                                                                                                                                                                                                                                                                         Query Match 46.9%; Score 1268.5; DB 15; Length 471; Best Local Similarity 57.2%; Pred. No. 5.1e-77; Matches 277; Conservative 37; Mismatches 85; Indels 85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196 PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173 QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH
                                                                                                                                                    117 EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 TLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 LTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKP
                                                                                        ---KTLSVS-----TWTCTVLQNQKK 192
                                                                                                                                                                                                     KILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP---LIIKNLKIEDSDTYICEVEDQKE
                                                                                                                                                                                                                                                 LLAVISGGQSQVPLVQSGTE----VKKPGASVNISCKAPGYTFTTFYMHWVRQAPGQGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRFTISRDLSKNMVFVQMGSLRAEDTAVYFCAKGNQPR-----VDIVASIEN---WGQG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNFPL---IIKN-----LKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQS 138
                                                                                                                        VVR-----GEDNYWGQGSLVIVSSASTKG--PSVFPLAPSSKSTSGGTAALGCLVKD
                                                                                                                                                                                     EWMGIRNP--SGRSSVSQKFEGRLTLTADTSTTTAHMELRNLTSDDTGVYYCTTTRWKW 122
                                                                                                                                                                                                                                                                                                         85; Indels 85; Gaps
                              247
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PRIOR APPLICATION NUMBER: PCT/US01/06191
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/184,601
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/254,465
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/254,498
PRIOR FILING DATE: 2000-12-08
PRIO
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Publication No. US20040043418A1
GENERAL INFORMATION:
APPLICANT: ELI LILLY AND COMPANY and WASHINGTON UNIVERSITY
TITLE OF INVENTION: Humanized Antibodies that Sequester Am
FILE REFERENCE: 8792/293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 274; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE: OTHER INFORMATION: Humanized antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 LGKKGDTVELTCTAS--QKKSIQFHWKNS-----NQIKILGNQGSF--LTKGPSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TFPAVLQSSGLYSLSSVVTVPSSSLGTQTVICNV--NHKPSNTKVD----KKVEPKSCDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG 136
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                                                                                                                                                                  PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
                                                                                                                                                                                                                                                                                          EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
                                                                                                                                                                                                                                                                                                                                                                                                                                  THTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----
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SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                         EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                                                                                                                                                                                                                                                                                                       THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-RDNAKNTLYLQMN-----SLRAEDTAVYYC-----ASGD---YWG
                                                                                                                                 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
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; Pred. No. 5.5e-77;
26; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 12;
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   441
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Sequence 2, Application US/10120198B
Publication No. US20030215427A1
GENERAL INFORMATION:
TITLE OF INVENTION: CET-SPECIFIC REDIRECTED IMMUNE CEI
FILE REFERENCE: 1954-337
CURRENT APPLICATION NUMBER: US/10/120,198B
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: 60/282,859
PRIOR FILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 11
RESULT 60
US-09-925-179-68
; Sequence 68, Application US/09925179
; Publication No. US20030044858A1
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US-10-120-198B-2
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SEQ ID NO 2
LENGTH: 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 VPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQF--HW---KNSNQI 59
                                                                                                                                                                                                         DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                                                                                                                                    YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                                                                                                                                                                                                                                                                      GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                 QLELQDSGTWTCT-----VLQNQXKVEFKIDIVPCPAPEPKSCDKTHTC----PELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DRVTITCKANEDINNRLAWYQQTPGNSPRLLISGATNLVTGVPSRFSGSGSGKDYTLTIT
                                                                                                                           RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                  YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                                                                                                                                                                                                                                                     GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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                                                                                                            RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                               DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
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                                                                                                              496
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GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
APPLICANTI Presta, Leonard G.
TITLE OF INVENTION: Anti-IgE Antibodies (as amended)
FILE REFERENCE: P0718P2CIDICIUS
CURRENT APPLICATION NUMBER: US/09/925,179

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Sequence 4, Application US/10423299
PUDIICATION NO. US20030229212A1
GENERAL INFORMATION:
APPLICANT: FAHRUER, ROBERT
APPLICANT: FOLLMAN, DEBORAH
APPLICANT: LEBRETON, BENEDICTE
APPLICANT: LVAN REIS, ROBERT
TITLE OF INVENTION: NON-AFFINITY PURIFICATION OF
PILE REFERENCE: 39766-0121A
CURRENT APPLICATION NUMBER: US/10/423,299
CURRENT FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: US 60/375,953
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                                                                                                                                                                                                                                          RESULT 61
US-10-423-299-4
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PRIOR APPLICATION NUMBER: US 08/466,163
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR PILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: PCT/US92/06860
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-08-14
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 273
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PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 68
SEQ ID NO 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Full-length heavy chain sequence corresponding to F(ab)9 of Tabl-09-925-179-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111
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                                                                                                                                                                                                                                                                                                                                                                                                                 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                           DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
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CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/256,164
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 9
LENGTH: 470
TYPE: PRT
ORGANISM: Artificial sequence
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; SEQ ID NO 4
; LENGTH: 451
; TYPE: PAT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is sy
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                                                                                                ; OTHER INFORMATION: US-10-020-786-9
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/10020786; Publication No. US20030073164A1
GENERAL INFORMATION:
APPLICANT: Simmons, Laura C.
APPLICANT: Rimowski, Laura
APPLICANT: Reilly, Dorothea
APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF
FILE REFERENCE: P1793R1
CURRENT APPLICATION NUMBER: US/10/020,786
CURRENT FILING DATE: 2002-03-26
DEPTOR ANTIFORMATION TO THE CONTROL OF THE CONTROL 
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Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                 FEATURE:
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58.9%; Pred. No. 7.2e
rative 28; Mismatches
46.9%;
Score 1266; DB 14; Pred. No. 7.6e-77;
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                              Length
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CURRENT APPLICATION NUMBER: US/10/227,694
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: US 60/315,209
PRIOR FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 5
LENGTH: 470
TYPE: PRT
ORGANISM: Artificial sequence
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US-10-227-694-5
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Best Local S
Matches 275
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publication No. US20030077739A1
GENERAL INFORMATION:
APPLICANT: Simmons, Laura
APPLICANT: Andersen, Dana
TITLE OF INVENTION: A SYSTEM FOR ANTIBODY
FILE REFERENCE: P1867R1
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                                                                                                                                                                                                                                                                                        FEATURE: OTHER INFORMATION: Synthetic
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                                                                                                                                    LVQPGGSLRLSCAASGFNIKEYYMHWVRQAPGKGLEWVGLIDPEQGN--TIYDPKFQDRA
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DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
                               -LOGOSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----
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                                                                                                                                                                                                   46.9%; Score 1266; DB 14; llarity 58.8%; Pred. No. 7.6e-77; Conservative 26; Mismatches 69;
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US-09-848-832-3

Sequence 3, Application US/09848832

Publication No. US20030165507A1

GENERAL INFORMATION:

APPLICANT: Hooper, Douglas

APPLICANT: Dietzschold, Bernhard

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS

FILE REFERENCE: HOO01.NP0002

CURRENT APPLICATION NUMBER: US/09/848,832

CURRENT FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: 60/204,518

PRIOR APPLICATION NUMBER: 60/204,518

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo
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KGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
                                                                          DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                             CDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
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                                                        DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
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APPLICANT: HOODER, Craig
APPLICANT: DIETZSCHOLD, Bernhard
TITLE OF INVENTION: Recombinant Antibodies, and
TITLE OF INVENTION: and Methods for Making Thr
FILE REFERENCE: 8321-110
CURRENT APPLICATION NUMBER: US/10/225,108A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US 09/848,832
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/204,518
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: US 60/314,023
PRIOR FILING DATE: 2001-08-21
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 3
LENCTH. 474
RESULT 66
US-10-461-148-1
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US-10-225-108A-3
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Best Local Similarity 59.1%;
Matches 276; Conservative 3
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ORGANISM: Homo
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 Application US/10461148
                                                                                                  SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                   KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
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                                                                                 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                  KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1266; DB 14;
Pred. No. 7.6e-77;
2; Mismatches 71;
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RESULT 67 US-10-207-655-240

Sequence 240, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25

FUSION

PROTEINS

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APPLICANT: HOODER, DOUGLAS C.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE SAME
FILE REFERENCE: 8321-110C11-185685
CURRENT APPLICATION NUMBER: US/10/461,148
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US 10/225,108
PRIOR FILING DATE: 2002-08-21
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/314,023
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 09/848,832
PRIOR APPLICATION NUMBER: US 09/848,832
PRIOR APPLICATION NUMBER: US 09/848,832
PRIOR APPLICATION NUMBER: US 60/204,518
PRIOR APPLICATION NUMBER: US 60/204,518
PRIOR FILING DATE: 2001-05-04
PRIOR TILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 474
TYPE: PRT
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Best Local Similarity
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427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 LVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSA--ISASGH-STYLADSVKGR
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SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                      SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                   KGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLD
                                                                                                     XGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
                                                                                                                                                                      DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
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Pred. No. 7.6e-77
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CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOPTWARE: PatentIn version 3.0
SEQ ID NO 398
LENGTH: 500
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
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ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion polypeptide
US-10-207-655-240
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                                  US-10-207-655-398
                                                                                                                                                                                                                                                                                                Sequence 398, Application US/10207655 Publication No. US20030118592A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn version
SEQ ID NO 240
LENGTH: 500
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Best Local Similarity
Matches 274; Conserv
Query Match
                                                                                                                                                                                                                           APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
                                                 OTHER INFORMATION: fusion polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                          SLSLSPG 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLSLSPG 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFSGSGSGTSYSLTISRVEAEDAATYYC----QQWSFNPPTFGAGTKLELKDGGGSGGGG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGL-------
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                                                                                                                                                                                                                                                      Jeffrey A.
 46.9%;
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Pred. No. 8.2e-77;
7; Mismatches 94;
 Score 1266;
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                                                          ; OTHER INFORMATION: US-10-071-485-67
                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/485,737
PRIOR FILING DATE: 2000-02-14
PRIOR PPLICATION NUMBER: PCT/EP 98/05165
PRIOR FILING DATE: 1998-08-14
PRIOR APPLICATION NUMBER: EPO 98870139.7
PRIOR APPLICATION NUMBER: EPO 97870122.5
PRIOR APPLICATION NUMBER: EPO 97870122.5
PRIOR FILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
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                                                                                                                                                                        SOFTWARE: PatentIn version 3.0 SEQ ID NO 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 67, Application US/10071485 Publication No. US20030099648A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 56.3%; Matches 274; Conservative :
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Buyse, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING
TITLE OF INVENTION: SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
FILE REFERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/10/071,485
CURRENT FILING DATE: 2002-07
                                                                                                                                      LENGTH: 468
TYPE: PRT
                                                                                              FEATURE:
                                                                                                                  ORGANISM: Artificial Sequence
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                                                                              SYNTHETIC
  46.8%;
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7; Mismatches 94;
Score 1265.5; DB 14; Pred. No. 8.1e-77;
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Query Match 46.8%; Score 1265.5; DB 14; Best Local Similarity 57.2%; Pred. No. 1.4e-76; Matches 277; Conservative 31; Mismatches 79; I
                                                                                                                                                             NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.0
SEQ ID NO 90
LENGTH: 711
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                                                                                                                                                                                                                               TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS FILE REFERENCE: INNS:015

CURRENT APPLICATION NUMBER: US/10/071,485

CURRENT FILING DATE: 2002-02-07

PRIOR APPLICATION NUMBER: 09/485,737

PRIOR FILING DATE: 2000-02-14

PRIOR PILICATION NUMBER: PC7/EP 98/05165

PRIOR FILING DATE: 1998-08-14

PRIOR APPLICATION NUMBER: EPO 98870139.7

PRIOR PILING DATE: 1998-06-18

PRIOR PILING DATE: 1998-06-18

PRIOR PILING DATE: 1998-08-18

PRIOR PILING DATE: 1997-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Buyse, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING
TITLE OF INVENTION: SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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CURRENT APPLICATION NUMBER: US/10/408,901; CURRENT FILING DATE: 2003-04-07; NUMBER OF SEQ ID NOS: 76; SOFTWARE: PatentIn version 3.0; SEQ ID NO 42; LENGTH: 445; TYPE: PRT; ORGANISM: Homo sapiens
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                                                                                                                                                            Query Match 46.8%; Score 1265; DB 16; Length 445; Best Local Similarity 59.0%; Pred. No. 8.2e-77; Matches 271; Conservative 27; Mismatches 71; Indels 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 42, Application US/10408901
Publication No. US20040023313A1
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Boyle, William
APPLICANT: Huang, Haichun
APPLICANT: Eliot, Robin
APPLICANT: Sullivan, John
APPLICANT: Medlock, Eugene
APPLICANT: Medlock, Eugene
APPLICANT: Martin, Francis
TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathwa;
TITLE OF INVENTION: Inhibitors
TITLE REFERENCE: MBHB 01-1145-A
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                                    82 SRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTL 141
                                                                                                                     34 GDTVELTCTASQ--KKSIQFHW-----KNSNQIKILGNQG----SFLTKGPSKLNDRAD
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                                                                               GGSLRLSCVGSRFTFSAYPMHWVRQAPGKGLEWVSGIGSGGGTNYADSVKGRFTIS-RDT
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  -SLRAEDMAVYYC-
ARGRNSFDYWGQGTLV
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US-10-411-037-56
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                                                                                                                                                                                    PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 56
LENGTH: 448
                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                   Matches
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA TITLE OF INVENTION: GALACTOSIDASE A FILE REFERENCE: 040853-01-5082
                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/411,037
                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/407,527
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                                                                                                                                                      TYPE: PRT
ORGANISM: Homo
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/404,249 FILING DATE: 2002-08-16
                                                                                                                                                                                                                                                                                                                             FILING DATE: 2002-07-17
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 13
                                 32 KKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG-----SFLTKGPSKLNDRADSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS------QLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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KPGSSVKVSCKASGYAFTNYLIEW-----VRQAPGQGLEWIGVIYPGSGGTNYNEKFKGR
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Bowe, Caryn
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Hakes, David
                                                                   Conservative
                                                                                                                                                      sapiens
                                                                                   46.8%;
58.7%;
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                                                                 Score 1265; DB 12;
Pred. No. 8.3e-77;
6; Mismatches 80;
                                                                                                 Length
                                                                                                    448;
                                                                   84;
                                                                   Gaps
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                                                                                                    ; ORGANISM: Homo US-10-411-026-56
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8
                                            Query Match
Best Local S
                                   Matches
                                                                                                                                      LENGTH: 44
TYPE: PRT
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270;

Similarity

46.8%; ilarity 58.7%; Conservative 26

26;

Score 1265; DB 12; Pred. No. 8.3e-77; 6; Mismatches 80;

Length Indels

448; 84;

Gaps

448

sapiens

32 KKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG-----SFLTKGPSKLNDRADSR 83

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GENERAL INFORMATION:
APPLICANT: Neose Technologies, I
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
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US-10-411-026-56
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                                                                                           FILE REFERENCE: 040853-01-553
CURRENT APPLICATION NUMBER: US/10/411,026
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR PRIOR DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
SOFTWARE: PatentIn version 3.2 SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 56, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE TITLE OF INVENTION: METHODS
                                                 NUMBER OF SEQ ID NOS:
                                                                         PRIOR FILING DATE: 2002-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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Hakes, David
Chen, Xi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
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40. US20040063911A1
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APPLICANT: Chen, X1

APPLICANT: Bowe, Caryn

TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND

TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF

FILE REFERENCE: 040853-01-5054

CURRENT APPLICATION NUMBER: US/0/410,962

CURRENT FILING DATE: 2003-04-09

PRIOR APPLICATION NUMBER: US 60/328,523

PRIOR FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR FILING DATE: 2001-10-19

PRIOR FILING DATE: 2001-10-19

PRIOR APPLICATION NUMBER: US 60/387,292

PRIOR APPLICATION NUMBER: US 60/387,292

PRIOR APPLICATION NUMBER: US 60/387,292

PRIOR FILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-25

PRIOR APPLICATION NUMBER: US 60/396,594

PRIOR FILING DATE: 2002-06-25

PRIOR APPLICATION NUMBER: US 60/396,594

PRIOR FILING DATE: 2002-06-25

PRIOR APPLICATION NUMBER: US 60/396,594

PRIOR FILING DATE: 2002-08-16

PRIOR FILING DATE: 2002-08-16
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US-10-410-962-56
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                                                                                          ; ORGANISM: Homo sapiens
US-10-410-962-56
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                                                                                                                                                          SOFTWARE: PatentIn version 3.2
SEQ ID NO 56
LENGTH: 448
Query Match 46.8%; Score 1265; DB 16; Best Local Similarity 58.7%; Pred. No. 8.3e-77; Matches 270; Conservative 26; Mismatches 80;
                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR PILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Neose Technologies,
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
                                                                                                                                       LENGTH: 44
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 LTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----QL
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Bayer, Robert
Hakes, David
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                                          Length
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  Indels
                                          448;
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Gaps
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TITLE OF INVENTION: ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON ALPHA: TITLE OF INVENTION: ALPHA
FILE REFERENCE: 040853-01-5055
CURRENT APPLICATION NUMBER: US/10/411,049
CURRENT APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/347,292
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/394,249
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR APPLICATION NUMBER: US 60/407,527
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PRIOR APPLICATION NUMBER: US 60/407,527
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PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR APPLICATION NUMBER: US 60/407,527
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Sequence 56, Application US/10411049
Publication No. US20040082026A1
GENERAL INFORMATION:
US-10-411-049-56
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                                                                                               NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn versi
SEQ ID NO 56
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APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
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APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
                                               LENGTH: 44
TYPE: PRT
                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                   PRIOR APPLICATION NUMBER: US 60, PRIOR FILING DATE: 2002-08-16, PRIOR APPLICATION NUMBER: US 60, PRIOR FILING DATE: 2002-08-28, NUMBER OF SEQ ID NOS: 75, SOFTWARE: Patentin version 3.2, SEQ ID NO 56
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                                                                                                                   PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILLING DATE: 2001-10-10
PRIOR PELICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILLING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILLING DATE: 2002-06-07
PRIOR PPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILLING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILLING DATE: 2002-08-16
PRIOR PRIOR PRIOR DATE: 2002-08-16
PRIOR PRIOR PRIOR DATE: 2002-08-16
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Matches
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                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/410,930
CURRENT FILING DATE: 2003-04-09
                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON TITLE OF INVENTION: BETA FILE REFERENCE: 040853-01-5056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Neose Technologies, Inc
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Similarity 58.7%;
70; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----QL
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Bowe, Caryn
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Hakes, David
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                                                                                                            60/407,527
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Pred. No. 8.3e-77;
86; Mismatches 80;
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APPLICANT: Neose Technologies,
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; ORGANISM: Homo sapiens US-10-410-930-56
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Best Local S
Matches 270
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                                                                                                          QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
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                       YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                               QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
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YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                           AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
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    448
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APPLICANT: Chen, Xi

APPLICANT: Bowe, Caryn
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF
TITLE OF INVENTION: FSH
FILE REFERENCE: 040853-01-5059
FULR REFERENCE: 040853-01-5059
CURRENT APPLICATION NUMBER: US/10/410,997
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR APPLICATION NUMBER: US 60/387,797
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR APPLICATION NUMBER: US 60/396,594
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PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
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Hakes, David
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Sequence 56, Application US/10411012
Publication No. US20040132640A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Edyer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Howe, Caryne
TITLE OF INVENTION: GLYCOPEGYLATION METHODS
FILE REFERENCE: 04083-01-5051
CURRENT APPLICATION NUMBER: US/10/411,012
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/347,292
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/396,594
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PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR APPLICATION NUMBER: US 60/404,249
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; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-997-56
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US-10-411-012-56
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Best Local Similarity 58.7%;
Matches 270; Conservative 26
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Pred. No. 8.3e-77;
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PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 56
LENGTH: 448
TYPE: PRT
ORGANIAM: Homo sapiens
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Matches 270; Conserv
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                      392 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                         349
                                                                                            332 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
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YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                         QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
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58.7%; Pred. No. 8.3e-77;
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RESULT 79
US-10-287-994-56
US-10-287-994-56
US-10-287-994-56
Publication No. US/20040137557A1
Publication No. US/20040137557A1
Publication No. US/20040137557A1
PERICANT: Neose Technologies, Inc.
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: DeFrees, Shawn
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
ITILE OF INVENTION, X
ITILE OF INVENTION, NUMBER: US/10/287,994
CURRENT FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/347,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249

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US-10-410-913-56
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FILE REFERENCE: 040853-01-5081
CURRENT APPLICATION NUMBER: US/10/410,913
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR PPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 56, Application US/10410913 Publication No. US20040142856A1 GENERAL INFORMATION:
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 62
                                                                                                                                                                                                                  APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: GLYCOCONJUGATION METHODS
TITLE OF INVENTION: METHODS
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APPLICANT: DeFrees, Shawn
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 391
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                                                                                                                                                                                                                                                                                                    Zopf, David
Bayer, Robert
Hakes, David
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; ORGANISM: Homo
US-10-410-913-56
                                                                                                           US-09-773-877A-18
                                                                                                                              RESULT 81
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             GENERAL INFORMATION:

APPLICANT: Xia, Yu-Ping et al.

TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
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Best Local Similarity 58.7%;
Matches 270; Conservative 2
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                                                                    Sequence 18, Application US/09773877A Publication No. US20030017977A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
FILE REFERENCE: REG 710b
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RESULT 81
US-09-773-877A-18
IS-09-773-877A-18
; Sequence 18, Application US/09773877A
publication No. US20030017977A1
; GENERAL INFORMATION:
   APPLICANT: Xia, Yu-Ping et al.
   TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN D.
   FILE REFERENCE: REG 710b
   CURRENT APPLICATION NUMBER: US/09/773,877A
   CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 27
   SOFTWARE: Patentin version 3.0
   SEQ ID NO 18
   LENGTH: 462
   TTYPE: PRT
   ORGANISM: Artificial Sequence
   FEATURE:
   OTHER INFORMATION: F1t1(2-3)-Fc (Mut3)
   US-09-773-877A-18
   Ouery Match
   Best Local Similarity 65.7%; Pred. No. 8.6e-77;
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US-09-773-877A-12
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Publication No. US20030017977A1

GENERAL INFORMATION:
APPLICANT: Xia, Yu-Ping et al.
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 710b
CURRENT APPLICATION NUMBER: US/09/773,877A
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOCTWARE: Patentin version 3.0
SEQ ID NO 12
LENGTH: 567
TYPE: NEW
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Best Local
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                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                           Local Similarity
                    284
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TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
                                                               SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
                                                                                                    DKMQNKDKGLYTCRVRSGPSFKSVNTSVHIYDKAGPGEPKSCDKTHTCPPCPAPELLGGP
                                                                                                                                                           PVKLLRGHTLVLNCTATTPLNTRVQMTWSYPDEKNKRASVRRRIDQSNSHANIFYSVLTI
                                                                                                                                                                                      DTHLLQGQSLTL--TLESPPGSSPSVQCRSPRGKNIQGG-----KTLSV 171
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                                              SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
                                                                                                                               SQLELQDSGTWTCTVLQNQ--KKVEFKIDIVPCPAP-EPKSCDKTHTC----PELLGGP 223
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 VFSCSVMHEALHNHYTQKSLSLSPG
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PRIOR APPLICATION NUMBER: 60/272,107
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-06-06
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 698
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: fusion construct US-09-875-338-9
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APPLICANT: CHANG, HAN
APPLICANT: FINGER, JOSH
APPLICANT: YANG, GUCHEN
APPLICANT: LU, PIN
APPLICANT: LU, VIN
APPLICANT: CHOU, XIA-DI
APPLICANT: PEACH, ROBER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ZHOU, XIA-DI
APPLICANT: PEACH, ROBERT
TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS
TITLE OF INVENTION: IMMUNOMODULATION
FILE REFERENCE: 3053-4071US2
CURRENT APPLICATION NUMBER: US/09/875,338
CURRENT FILING DATE: 2001-06-06
                                                                                                                                                                                                                                                                                                                   179 SGTWTC----TVLQNQKKVEFKIDIVPCPAP---EPKSCDKTHTC-----PELLGGPSVF
                                                                                                                                                                                                                                                                                        433 NGTYSCLVRNPVLQQDAHGSVTITGQPMTFPPEFEPKSCDKTHTCPPCPAPELLGGPSVF
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                                             QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
                                                                                          VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                                      VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                                                                                                        LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
                                                                                                                                                                                                                   LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
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673 VFSCSVMHEALHNHYTQKSLSLSPG

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RESULT 85
US-09-773-877A-20
; Sequence 20, Application US/09773877A
; Publication No. US20030017977A1
; GENERAL INFORMATION:
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Publication No. US200
GENERAL INFORMATION:
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Best Local Similarity
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PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/209,811
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 138
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: PEACH, ROBERT
TITLE OF INVENTION: B7-RELATED NUCLEIC ACIDS AND
TITLE OF INVENTION: IMMUNOMODULATION
FILE REFERENCE: 3053-4071US3
CURRENT APPLICATION NUMBER: US/10/077,023
CURRENT FILING DATE: 2002-02-15
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NGTYSCLVRNPVLQQDAHGSVTITGQPMTFPPEFEPKSCDKTHTCPPCPAPELLGGPSVF
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No. US20030031675A1
                                                                                                                                                           VFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                               QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
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                                                                                                                                     VFSCSVMHEALHNHYTQKSLSLSPG
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HUSE, William D.

APPLICANT: Wu, Herren
APPLICANT: Watkins, Jeffry D.
ITITLE OF INVENTION: High Potency Recombinant Antibodies and Methods of
TITLE OF INVENTION: Producing Them
FILE REFERENCE: 469201-526
CURRENT APPLICATION NUMBER: US/09/796,848A
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: U.S. 60/186,252
PRIOR APPLICATION NUMBER: U.S. 60/186,252
PRIOR FILING DATE: 2000-03-01
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 37
LENGTH: 450
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US-09-796-848A-37
; Sequence 37, Application US/09796848A
; Patent No. US20020098189A1
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CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
LENGTH: 567
TYPE: PRT
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TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
FILE REFERENCE: REG 710b
                    ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Heavy chain
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; Pred. No. 1.3e-76;
23; Mismatches 72;
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FILE REFERENCE: 469201-526
CURRENT APPLICATION NUMBER: US/09/796,848A
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: U.S. 60/186,252
PRIOR FILING DATE: 2000-03-01
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 45
LENGTH: 450
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 87
US-09-796-848A-45
, Sequence 45, Application US/09796848A
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                                                                                                           ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: high potency antibody.
US-09-796-848A-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. US20020098189A1 GENERAL INFORMATION:
                                      Matches 271;
                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity Matches 271; Conserv
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Young, James F.
APPLICANT: Johnson, Leslie S.
APPLICANT: Huse, William D.
APPLICANT: Wu, Herren
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: High Potency Recombinant Antibodies
TITLE OF INVENTION: Producing Them
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30 LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL-----NDRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSRRSLWD-----QGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
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                                   46.8%;
ilarity 57.8%;
Conservative 2:
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                                    27; Mismatches
                                 Score 1263.5; DB 9;
Pred. No. 1.1e-76;
27; Mismatches 74;
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US-09-996-288-220
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SOFTWARE: Patentin version 3.1
SEQ ID NO 220
LENGTH: 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 220, Application US/09996288 Patent No. US20020177126A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
  167
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                                                                                                             132 HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----
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                                                                                                                                                      60 DYNPSIKDRLTISKDTSKNQVVLKVTNMDPADTATYYCARD-----MIFNFYFD---
                                                                                                                                                                                                                                   11 LVKPTQTLTLTCTFS-----GFSLSTAGMSVGWIRQPPGKALEWLADIWWDGKK
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                                                                                                                                                                                                                                                                                                                                   Similarity
TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP
                                      -----QLELQDSG-----
                                                                         -- VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL
                                                                                                                                                                                        DSRRSIWD------QGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----
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                                                                                                                                                                                                                                                                                                            46.8%; Score 1263.5; DB llarity 57.8%; Pred. No. 1.1e-76; Conservative 27; Mismatches 74
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                                    ----TWTCTVLQNQKKVEFKIDIVPCPAPEP
                                                                                                                                                                                                                                                                                                                                                   DB 9;
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                                                                                                                                                                                                                                                                                                            97;
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220
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APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for
TITLE OF INVENTION: and Treatment
TITLE OF INVENTION: and Treatment
TILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.1
SEQ ID NO 226
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-09-996-288-226
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US-09-996-288-226
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Best Local Similarity
Matches 271; Conserv
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                                                          KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                      YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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US-09-996-288-232
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US-09-996-288-232
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APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.1
SEQ ID NO 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 232, Application Patent No. US20020177126A1 GENERAL INFORMATION:
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ORGANISM: Homo
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                    LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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                                                                                                  KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                                                                    YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSRRSL-----WDQGNFPLIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
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LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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57.8%; Pred. No. 1.1e-76;
tive 27; Mismatches 74
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RESULT 91

US-09-996-288-234

Sequence 234, Application US/09996288

Patent No. US20020177126A1

GENERAL INFORMATION:

APPLICANT: Young, James
APPLICANT: Scott, Koenig

APPLICANT: Leslie, Johnson

TITLE OF INVENTION: Methods of Adminstering/Dosing.
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999

CURRENT APPLICATION NUMBER: US/09/996,288

CURRENT FILING DATE: 2001-11-28

Anti-RSV Antibodies for Prophylaxi

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Sequence 236, Application US/09996288

Patent No. US2002017126A1

GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
ITILE OF INVENTION: Methods of Adminstering/Dosing Ant
FILE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999

CURRENT APPLICATION NUMBER: US/09/996,288

CURRENT FILING DATE: 2001-11-28

NUMBER OF SEQ ID NOS: 259

SOFTWARE: PStentIn version 3.1

SEQ ID NO 236

LENGTH: 450

Type: PAT
ORGANISM: Homo sapiens

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US-09-996-288-234
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SOFTMARE: PATENTIN VERSION
SEQ ID NO 234
LENGTH: 450
TYPE: PRT
                                                                               Query Match
Best Local Similarity
Matches 271; Conserv
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      LVKPTQTLTLTCTFS------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK
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                                          LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL-----NDRA
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                                                                               46.8%; Score 1263.5; DB 9; ilarity 57.8%; Pred. No. 1.1e-76; Conservative 27; Mismatches 74;
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                                                                                                                        Length
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APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: methods of Adminstering/Dosing Ant
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION UNMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.1
SEQ ID NO 238
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-996-288-238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                           81 DSRRSL------WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
                                                                                                                                                                                                                                                                                                  11 LVKPTQTLTLTCTFS------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK
KSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                           TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEP
                                                                                                                                           --VWGQGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL
                                                                                                                                                                                                                      DYNPSLKSRLTISKDTSKNQVVLKVTNMDPADTATYYC----ARDMITNFYFD-----
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                                                                                                    ----QLELQDSG----
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                                                                                                    ----TWTCTVLQNQKKVEFKIDIVPCPAPEP
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US-09-996-288-242
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Patent No. US30020177126A1

GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Scott, Koenig
APPLICANT: Itelie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOPTWARE: Patentin version 3.1
SEQ ID NO 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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                   LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                    KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                   YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                      YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVKPTQTLTLTCTFS------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK
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LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                  KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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Sequence 244, Application US/09996288
Patent NO. US20020177126A1
GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing And
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION UMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
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US-09-996-288-244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 46.8%;
Best Local Similarity 57.8%;
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                LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                                YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                               KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                              YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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Pred. No. 1.1e-76;
6; Mismatches 75;
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Sequence 246, Application Patent No. US20020177126A1 GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV.
TITLE OF INVENTION: and Treatment
TILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                          Antibodies
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RESULT 96 US-09-996-288-246

US/09996288

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Sequence 252, Application US/0996288

Patent No. US20020177126A1

GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Ant
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION UNMBER: US/09/996,288
CURRENT APPLICATION UNMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.1
SEQ ID NO 252
LENGTH: 450
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; ORGANISM: Homo sapiens
US-09-996-288-246
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                                                                                   Query Match
Best Local Similarity
Matches 271; Conserv
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                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
-09-996-288-252
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LENGTH: 450
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DSRRSLWD-----QGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
                           LVKPTQTLTLTCTFS------GFSLSTAGMSVGWIRQPPGKALEWLADIWWDDKK 59
                                                      LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL------
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                                                                                     46.8%; Score 1263.5; DB 9; Length ilarity 57.8%; Pred. No. 1.1e-76; Conservative 27; Mismatches 74; Indels
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GENERAL INFORMATION:

APPLICANT: Young, James

APPLICANT: Scott, Koenig

APPLICANT: Scott, Koenig

APPLICANT: Leslie, Johnson

TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Ant:

TITLE OF INVENTION: and Treatment

FILE REFERENCE: 107271-047-999

CURRENT APPLICATION NUMBER: US/09/996,288

CURRENT APPLICATION NUMBER: US/09/996,288

CURRENT FILING DATE: 2001-11-28

NUMBER OF SEQ ID NOS: 259

SOFTWARE: PatentIN version 3.1

SEQ ID NO 254

LENGTH: 450

TYPE: PRT

ORGANISM: Homo sapiens

US-09-996-288-254
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US-09-996-288-254
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US-09-996-288-256
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APPLICANT: Scott, Koenig
APPLICANT: Lealie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: PatentIn version 3.1
SEQ ID NO 256
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local S
Matches 271
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Local Similarity 57.8%; Pred. No. 1.1e-76;
les 271; Conservative 27; Mismatches 74; Indels 97;
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Sequence 220, Application US/09996265
Publication No. US20030091584A1
GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Young, James
APPLICANT: Leslie, Johnson
TITLE OF INVENTION:
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
TITLE OF INVENTION: And Treatment
FILE REFERENCE: 10271-048-99
CURRENT APPLICATION UNMERS: US/09/996,265
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 220
LENGTH: 450
TYPE: PRT
CRCANISM: Homo sapiens
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                      LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                               KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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Search completed: August 3, 2004, 13:48:10 Job time : 51.3363 secs

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Perfect score:
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Listing first 125 summaries
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Aar26530 Sequence
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220. .329
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330. .436
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Matches 425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 435 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD4-gamma 1 chimeric heavy chain homo-dimer and its expression vector for preventing and treating HIV infection useful as a diagnostic agent
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LHNHYTQKSLSLSPG 431
                                                                                                                                                                                 MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
                                                                                                                                                                                                       MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
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                                                                  FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
                                                                                                                                     DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
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                                               FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
                                                                                                                 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
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97.7%;
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Pred. No. 3.9e-115;
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RESULT 2
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420

LHNHYTQKSLSLSPG

434

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Human; CD4; cluster of differentiation factor 4; immunoglobulin; Ig; human immunodeficiency virus; gene therapy; vaccine; HIV-1 infection; D2; alpha tailpiece; alphatp; fusion protein.
Homo sapiens
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WO2003040311-A2

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a CD4 (cluster of differentiation factor 4) polypeptide ligated at its C-terminus with a portion of an immunoglobulin (Ig) comprising a hinge region and a constant domain of a mammalian Ig heavy chain. The polypeptide comprises a tailpiece from the C-terminus of the heavy chain of an IgA or IgM antibody. Polypeptides of the invention are useful for preparing a composition for treating or preventing human immunodeficiency virus (HIV)-1 infection. The invention is useful in gene therapy and also in the preparation of vaccines. The present sequence is a fusion protein which comprises a human IgA alpha tailpiece (alphatp), a human IgC constant region comprising a hinge, a CH2 and CH3 region and a human CD4 DID2 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New CD4 polypeptide ligated at its C-terminus with a portion of immunoglobulin, useful for preparing a composition for treating preventing HIV-1 infection.
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DB; AAD29113.
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                                                                                                      ALHNHYTOKSLSLSPG-----LQLDETC
                                                                                                                                   GFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
                                                                                                                                                    GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 415
                                                                                                                                                                                               QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                          ALHNHYTOKSLSLSAGKPTHVNVSVVMAEVDGTC
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93.2%;
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Pred. No. 1.4e-113;
2; Mismatches 8;
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AAR26531 standard; protein; 534

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Matches 428
                                                                                                                                                                                                                           The human CD4 cDNA is excised from the plasmid pSP674 and cloned into M13mp18. In order to excise a fragment containing the CH1 exon of the human gamma 1 heavy chain gene, the plasmid pBr gamma 1 is digested with SacII, and the SacII sites are then made flush using T4 DNA polymerase. The fragment containing the CH1 exon is then purified and ligated to the M13mp18 (CD4) vector. Oligonucleotide-mediated site-directed mutagenesis is then performed to juxtapose the CD4 and CH1 sequences in frame. The CD4-CH1 chimeric gene is then linearized and ligated to the Pst1-Pst1 DNA fragment of the plasmid pBr gamma 1 containing the hinge, CH2, and CH3 exons of the human gamma 1 chain gene designated CD4-IgGIHC-pRcCMV (ATCC 75192). (Updated on 25-MAR-2003 to correct PN field.)
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28-JAN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-FEB-1991;
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Similarity 80.3%;
28; Conservative
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LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                                                                                                                                      4; 88pp; English.
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bel= CH2
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                                                                                                                                                   Score 2176; DB 2;
Pred. No. 8.1e-113;
0; Mismatches 3;
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RESULT 4

ARE37127 4

ARE37127 6

ID ARE32

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XX 47-A

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XX Huma

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FT Misc

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The invention relates to a CD4 (cluster of differentiation factor 4) polypeptide ligated at its C-terminus with a portion of an immunoglobulin (Ig) comprising a hinge region and a constant domain of a mammalian Ig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; CD4; cluster of differentiation factor 4; immunoglobulin; Ig; human immunodeficiency virus; gene therapy; vaccine; HIV-1 infection; D2; alpha tailpiece; alphatp; fusion protein; mutein; variant; mutant
                                                                                                                                                     New CD4 polypeptide ligated at its C-terminus with immunoglobulin, useful for preparing a composition preventing HIV-1 infection.
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                                                                                                     Example 11;
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                                                                                                                                                                                                                                                                                                                                    Cicala C,
                                                                                                                                                                                                                                                                                                                                                                                          DEPT HEALTH & HUMAN SERVICES
                                                                                                     Page 67; 100pp; English.
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Best Local Sim
Matches 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heavy chain. The polypeptide comprises a tailpiece from the C-terminus of the heavy chain of an IgA or IgM antibody. Polypeptides of the invention are useful for preparing a composition for treating or preventing human immunodeficiency virus (HIV)-1 infection. The invention is useful in gene therapy and also in the preparation of vaccines. The present sequence is a fusion protein variant (G218P/L219V/220de1A/G221A) which comprises a human IgA alpha tailpiece (alphatp), a human IgA2 constant region comprising a hinge, a CH2 and CH3 region and a human CD4 D1D2 domain. This variant protein is also referred to as mutant F
                                                                                                                                                                                               Genetic construct which encodes CD4 linked to human IgG1 at the Esp upstream of the hinge region (fusion protein CD4E-gamma-1).
                                                                                                                                                    Fusion protein;
diagnosis; CD4;
                                                                                                                                                                                                                                               25-MAR-2003
02-NOV-1992
                                                                                                                                                                                                                                                                                                                           AAP93009 standard;
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22-JAN-1988;
                                                            26-JUL-1989
                            20-JAN-1989;
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 88US-00147351
                              89EP-00100913
                                                                                                                                                   gp120;
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gp120; binding fragment; glycoprotein; variable
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N-PSDB; AAN90357.
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WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                               ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                                                  NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
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                                       ELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                       NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TWTCTVLQNQKKVEFKI DI VVLAFQKASSI VYKKEGEQVEFSFPLAFTVEKLTGSGELWW
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67.8%;
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Pred. No. 5.4e-110;
D; Mismatches 4;

    used for treating HIV in sample.

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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                                                                                The present sequence is that of fusion protein CD4Egammal comprising the extracellular portion of CD4, which binds to HIV gpl20, linked at its C-terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA encoding CD4 was linked to IgG1 DNA at the Esp site upstream of the hinge region (see AAA50661). Fusion protein CD4Egammal and a nucleic acid encoding it are claimed. Also claimed are a vector comprising the nucleic acid, and a method of producing the fusion protein in secreted form using a transformed host cell. The fusion protein may further comprise a therapeutic agent, radiolabel or NMR imaging agent. The fusion protein can be administered to an animal (including humans) for treatment of HIV or SIV infection, and can also be used in assays for HIV or SIV, imaging and tissue stains. IgG1 fusion proteins such as CD4Egammal provide both complement-mediated and cell-mediated immunity
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gp120; therapy;
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89US-00299596.
92US-00896781.
93US-00057952.
94US-00191708.
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Score 2126.5;
Pred. No. 5.4e-
0; Mismatches
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusion protein; human; CD4; IgG1; anti-human immunodeficiency virus;
WPI; 2000-085792/07
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                                                                                                                                                                                                                                                                                               21-DEC-1999
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                                                                                          GEN
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89US-00299596.
92US-00896781.
93US-00057952.
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WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                                GPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKFREEQY
                                                                                                                                                                                                     LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEEPKSCDKTHTCPPCPAPELLG
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                                                                                                 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                   GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
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                                                                                                                                                                                                                                                                                                    QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fusion gene encoding immunoglobulin-CD4 fusion proteins, use treatment of HIV or simian immunodeficiency virus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-063015/06.
DB; AAZ48202.
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                                                                                                                                                                                                                                                                                                           MRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                       TWTCTVLQNQKKVEFKIDIV-----
                                                                                                                                                                                           LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                       MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQPHWKNSNQIK
LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                       LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                       QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                 TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
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                                                                                                                                                                                                                                                                                                                                                  78.7%;
nilarity 67.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                Score 2126.5; DB 3; Pred. No. 5.4e-110; 0; Mismatches 4;
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25-MAR-2003
06-FEB-1993
                                                                         CD4-gamma-2 and CD4-IgG2 chimera(s) treatment, prevention and diagnosis
                                                          Claim
                                                                                                  WPI; 1992-300034/36.
N-PSDB; AAQ28088.
                                                                                                                             Beaudry GA,
                                                                                                                                                              08-FEB-1991;
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                                                                                                                                                                                                                                                                                                      Chimeric
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                                                                                                                                                                                                                                                                                                                                                       CD4-gamma2
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                                                                                                                                                                                                                                                                                                                               increased
                                                                                                                                                                                                                                                                                                                              soluble CD4; T cell receptor; increased serum half life; HIV
                                                                                                                                                                                                                                                                                                                                                        chimeric heavy chain homodimer.
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(revised)
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217. .325
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                                                                          and expression vectors of HIV infection.
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                                                                                                                                                                                                                                                                                                                               CD4 antigen; high recovery; infection; AIDS; ss.
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was produced by expression of the coding mutagenised cDNA (produced as described in AAQ28088) in Dhfr-CHO cells. The protein is efficiently assembled intracellularly and effectively secreted from mammalian cells pref. CHO, COS, or myeloma cells as a homodimer, enabling high recovery and purification from the medium of cells expressing it. It possesses

represents a CD4-gamma2

chimeric heavy chain homodimer.

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AAR46678
ID AAR46
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CX CD4;
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Best Local (
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                                                                                                                                                                                                                                                           25-MAR-2003
08-AUG-1994
                                                                    Region
                                                                                                                                           Homo sapiens
                                                                                                                                                                                                    CD4; gamma;
                                                                                                                                                                                                                                CD4-gamma 2
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                                                                                                                                                                                     immunodeficiency virus; radionuclide; toxin; therapy; treatment;
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                                                                                                                                                                                                                                                                                                                                standard; protein; 432
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                                                                                                                                                                                                  heavy chain; chimeric; chimaeric; immunoconjugate; HIV;
                                                                                                                                                                                                                                chimeric heavy chain.
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No. 6.4e-110;
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Matches 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2 immuno:conjugates - used to kill HIV-infected cells and to image HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 432 AA;
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N-PSDB; AAQ57750.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                            VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
                                                                                                                     VSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ
                                                                                                                                      VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ
                                                                                                                                                                                                                                                                          TWTCTVLQNQKKVEFKIDIV-------PCPAPEPKSCDKTHTCPELLGGPSVFL
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FSCSVMHEALHNHYTQKSLSLSPG
                 FSCSVMHEALHNHYTQKSLSLSPG
                                                          VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNV
                                                                                                                                                                                 FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRV
                                                                                                                                                                                               FPPKPKDTLMISRTPEVTCVVVDVSHEDÞEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
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Pred. No. 6.4e-110;
8; Mismatches 5;
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                                                                                                                                                                                                                                  immunoconjugate comprising a cytotoxic radionuclide and a heterotetramer CC of two heavy chains and two light chains. The cytotoxic radionuclide is CC linked to either the heavy chains or the light chains, or to all four CC chains, directly or through a bifunctional chelator. Both heavy chains CC are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by vector CD4- [CC chains encoded by vector CD4- kLC-pRcCMV (ATCC 75194). CD4 is a non-CC chains encoded by vector CD4- kLC-pRcCMV (ATCC 75194). CD4 is a non-CC chains encoded by vector CD4- kLC-pRcCMV (ATCC 75194). CD4 is a non-CC chains encoded by vector CD4- kLC-pRcCMV (ATCC 75194). CD4 is a non-CC chains encoded by vector CD4- kLC-pRcCMV (ATCC 75194). CD4 is a non-CC chains encoded by vector CD4- klc-pRcCMV (ATCC 75194). CD4 is a non-CC chains encoded by vector CD4- klc-pRcCMV (ATCC 75194). CD4 is a non-CC chains encoded by vector CD4- klc-pRcCMV (ATCC 75194). CD4 is a non-CC chains encoded by vector CD4- klc-pRcCMV (ATCC 75194). CD4 is a non-CC chains encoded by vector CD4- klc-pRcCMV (ATCC 75194). CD4 is a non-CC chains encoded by vector CD4- klc-pRcCMV (ATCC 75194). CD4 is a non-CC chains encoded by vector CD4- klc-pRcCMV (ATCC 75194). CD4 is a non-CC chains encoded by vector CD4- klc-pRcCMV (ATCC 75194). CD4 is a non-CC chains encoded by vector CD4- klc-pRcCMV (ATCC 75194). CD4 is a non-CC chains encoded by vector CD4- klc-pRcCMV (ATCC 75194). CD4 is a non-CC chains encoded by vector CD4-klc-pRcCMV (ATCC 75194). CD4 is a non-CC chains encoded by vector CD4-klc-pRcCMV (ATCC 75194). CD4 is a non-CC chains encoded by vector CD4-klc-pRcCMV (ATCC 75194). CD4 is a non-CC chains encoded by vector CD4-klc-pRcCMV (ATCC 75194). And the surface of a line encoded by vector CD4-klc-pRcCMV (ATCC 75194). And the surface of a line encoded by vector CD4-klc-pRcCMV (ATCC 75194). And the surface of a line encoded by vector CD4-klc-pRcCMV (ATCC 75194). And the surface of a line encoded by vector CD4-klc-pRcCMV (ATCC 75194). And the surface of a line encoded by vector CD4-klc-p
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06-AUG-1993;
03-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New immunoconjugate, used to treat, prevent or image human immune deficiency virus infection, comprises radionuclide attached to heterotetramer of CD4-immunoglobulin chimeras.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAR-2000
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                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the human CD4-gamma 2 chimeric heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 3; 58pp; English.
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93WO-US007422.
95US-00379516.
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Score 2122; DB 3;
Pred. No. 6.4e-110;
B; Mismatches 5;
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                                                                       Length 432;
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Conservative

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The present invention relates to an immunoconjugate, comprising a cytotoxic radionuclide linked, directly or via a bifunctional chelator,

Fig

3; 43pp;

English

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06-AUG-1993;
03-FEB-1995;
07-JUN-1995;
                                                   Immunoconjugate for treating human immunodeficiency virus-infected subject, consists of cytotoxic radionuclide linked to heterotetrame comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4-kappalight chains.
                                                                                                                                                                                                                                                                               US6177549-B1
                                                                                                                                                                                                                                                                                                                                                CD4-gamma2 chimeric heavy chain homodimer protien
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                                                                                                                                                        (PROG-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNV
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93WO-US007422.
95US-00379516.
95US-00477460.
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                                                                                                                                                                                                                                                                                                                           chelator; chimeric; HIV; human immunodeficiency virus
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                                                               to heterotetramer
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RESULT 13
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Best Local Similarity
                                            08-FEB-1991;
10-FEB-1992;
08-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to a heterotetramer having two chimeric CD4-IgG2 heavy chains encoded an expression vector CD4-IgG2HC-pRcCMV and two chimeric CD4-kappa ligh chains encoded by an expression vector CD4-kLC-pRcMV. The invention is useful for killing human immunodeficiency virus (HIV)-infected cells, the treatment and prevention of infection with HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Maddon
                                                                                          07-JUN-1995;
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                                                                                                                                                                                 1mmunoglobulin
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                      (PROG-) PROGENICS PHARM INC
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                                                                                                                                                                                             Anti-HIV; CD4-IgG2
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                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                                                                 FSCSVMHEALHNHYTQKSLSLSPG
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                                           91US-00653684.
92WO-US001143.
92US-00960440.
                                                                                                                                                                                  gamma
                                                                                          95US-00485372
                                                                                                                                                                                                                   chimeric heavy chain homodimer.
                                                                                                                                                                                                                                                                                       protein;
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                                                                                                                                                                                              chimeric heterotetramer;
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Pred. No. 6.4e-110;
8; Mismatches 5;
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                                      The present invention relates to a method for inhibiting infection of a CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2 chimeric heterotetramer to form a complex with the HIV (CD4 = cluster of differentiation 4; IgG2 = immunoglobulin gamma 2). CD4 is a cell surface glycoprotein that is expressed primarily on the surface of T cells. In man, CD4 is the target of interaction with HIV. The heterotetramer has two heavy and two light chains which are encoded by expression vectors CD4-IgG2HC-pRcCMV (VI) and CD4-KLC-pRcCMV (V2), respectively. The method is used to inhibit infection of a CD4+ cell by a HIV and to prevent CD4+cells of a subject from becoming infected with HIV. The method is also useful for treating a subject having CD4+ cells infected with HIV. The present sequence is human fusion protein: CD4-gamma2 chimeric heavy chain homodimer. This sequence was used in the method of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-264981/27.
N-PSDB; AAF77829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting human immunodeficiency virus or treating a subject having CD4+ cells CD4-IgG2 chimeric heterotetramer to form
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Sequence 432 AA;

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                                                                  VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNV
                                                                                                                         VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ
                                                                                                                                                                FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRV
                                                                                                                                                                               FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
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                                                       VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNV
                                                                                                           VSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQ
                                                                                                                                                                                                                    TWTCTVLQNQKKVEFKIDIVVLAFERKCCVECPPCPAPP-----VAGPSVFL
                                                                                                                                                                                                                                              TWTCTVLQNQKKVEFKIDIV-------PCPAPEPKSCDKTHTCPELLGGPSVFL
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91.2%;
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Pred. No. 6.4e-110;
B; Mismatches 5;
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ABG71122

protein;

17-JAN-2003

(first entry)

CD4-gamma2 chimeric heavy chain

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CD4-IgG2 chimeric

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Query Match
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10-FEB-1992;
08-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                             The invention describes a purified CD4-immunoglobulin (Ig)G2 chimeric heterotetramer (I) that neutralises human immunodeficiency virus-1 (HIV-1) having two heavy chains encoded by an expression vector designated CD-1gG2HC-pRcCMV. (I) light chains encoded by expression vector designated CD4-kLC-pRcCMV. (I) and a composition (II) comprising (I) or (II) inked to a toxin, are useful for inhibiting HIV infection of a CD4 cell, and preventing a subject being infected with HIV by blocking the spread of HIV infection. This is the amino acid sequence of the CD4-gamma2 chimeric heavy chain of the CD4-IgG2 chimeric heterotetramer useful in inhibiting HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel CD4-immunoglobulin G2 chimeric heterotetramer neutralizes human immunodeficiency virus-1 with two heavy and light chains encoded by expression vectors designated CD4-IgG2HC-pRcCMV and CD4-kLC-pRcCMV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                     Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
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DB; ABS55720.
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                                                                                                                               LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                     FPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRV
                                                                       TWTCTVLQNQKKVEFKIDIV-----
                                                                                                               LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                        ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                                                 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                        TWTCTVLQNQKKVEFKIDIVVLAFERKCCVECPPCPAPP-
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91.2%;
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Pred. No. 6.4e-110;
B; Mismatches 5;
                                                                                   PCPAPEPKSCDKTHTCPELLGGPSVFL
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25-MAR-2003
06-FEB-1993
This sequence represents a CD4-IgG2 chimeric heavy chain heterotetramer It was produced by expresion of the coding mutagenised cDNA (produced as described in AAQ28089) in Dhfr-CHO cells. The protein is efficiently assembled intracellularly and effectively secreted from mammalian cells pref. CHO, COS, or myeloma cells as a heterotetramer, enabling high recovery and purification from the medium of cells expressing it. It possesses increased serum half-life and has increased avidity for HIV cf. heavy chain dimers. It can inhibit HIV infection of CD4+ cells and block the spread of HIV infection within a patient. Attachment to a detectable
                                                                                                                                                                                                                                                                                             CD4-gamma-2 and CD4-IgG2 chimera(s) treatment, prevention and diagnosis
                                                                                                                                                                                                                                                  Claim 15;
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                                                                                                                                                                                                                                                Fig 4; 90pp;
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                                                                                                                                                                                                                                                                                                                             cytotoxic radionuclide; cell surface glycoprotein; prevent; infection; cellular immune response interaction mediator; HIV interaction; staging;
07-AUG-1992;
06-AUG-1993;
                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                   prognosis; envelope glycoprotein
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92US-00927931.
93WO-US007422.
                                                                                  95US-00477460
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77.3%;
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Pred. No. 8.9e-108;
9; Mismatches 13;
                                                                                                                                                                                                                                                                                                         burden;
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TVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW ----KSCDKTHTCP-ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW

VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDK

300 207 240 밁 S 밁 á

Query Match Best Local Similarity Matches 409; Conser

Conservative

9;

77.2**%**; 77.3**%**;

Score 2085; DB 3; Pred. No. 8.9e-108; 9; Mismatches 13;

Length Indels

530; 98;

Gaps

4;

Sequence

530

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LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG

TWTCTVLQNQKKVEFKIDIV-----PEPA-----PCPA------PEP LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG

TWTCTVLQNQKKVEFKIDIVVLAFASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP

ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120

ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL

120

180 180

207

MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK

MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK

60

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This sequence represents the CD4-IgG2 chimeric heavy chain amino acid compenses of the computation of the computation of the computation of the invention relates to an immunoconjugate computation and two light chains. The cytotoxic compensation of the computation of the light chains or the light chains, or compensation of the light chains or the light chains, or compensation of the light chains, or compensation of the light chains, or compensation of the light chains, or compensation of the light chains or the light chains, or compensation of the light chains are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by vector CD4-Ig (immunoglobulin) G2 chains encoded by vector CD4-Ig (immunoglobulin) G2 chains encoded by vector CD4-Ig (immunoglobulin) G2 chains encoded by compensation of the monocyte/macrophage lineage composition of the monocyte/macrophage lineage composition of the composition of the monocyte/macrophage lineage composition of the surface of antigen presenting cells to complex (MHC) class II molecules on the surface of antigen presenting cells to complex composition of interactions with the human immunodeficiency virus HIV. The complex composition of interaction infected with HIV, and for treating composition or prognosis of infection, and for assessing efficacy of complex composition or prognosis of infection, and for assessing efficacy of communoconjugate is also used for imaging HIV-infected tissues (for staging and prognosis of HIV infected patients. The immunoconjugate should be active against all strains of HIV (since the CC dimense) interaction is essential for infection). The heterotetramers communicated intracellularly and secreted efficiently from mammalian collings high recovery and purification from the culture medium. They have longer half-life in serum and greater avidity than heavy chain collings the collings of the collings of the collings of the collings of the collings of the collings of the collings of the collings of the collings of the collings of the collings of the collings
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 4; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New immunoconjugate, used to treat, prevent or image human immune deficiency virus infection, comprises radionuclide attached to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heterotetramer of CD4-immunoglobulin chimeras.
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RESULT 17
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Best Local Sim
Matches 409;
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06-AUG-1993;
03-FEB-1995;
07-JUN-1995;
                                                                                                                                                                           The present invention relates to an immunoconjugate, comprising a cytotoxic radionuclide linked, directly or via a bifunctional chelator, to a heterotetramer having two chimeric CD4-IgG2 heavy chains encoded by an expression vector CD4-IgG2HC-pRcCMV and two chimeric CD4-kappa light chains encoded by an expression vector CD4-kG-pRcMV. The invention is useful for killing human immunodeficiency virus (HIV)-infected cells, for the treatment and prevention of infection with HIV
                                                                                                                                                                                                                                                                                                          Immunoconjugate for treating human immunodeficiency virus-infected subject, consists of cytotoxic radionuclide linked to heterotetramer comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4-kappalight chains.
                                                                                                                                                       Sequence 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD4-IgG2 chimeric
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                                                                                                                Similarity
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              ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                              MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKS1QFHWKNSNQIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
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ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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93WO-US007422.
95US-00379516.
95US-00477460.
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                                                                                                             77.2%;
77.3%;
                                                                                                 9; Score 2085; DE
9; Mismatches
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                                                                                                  e 2085; DB 4;
. No. 8.9e-108;
ismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human immunodeficiency virus.
                                                                                                                         Length 530;
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                                                                                                                                                                                                                                                                                                                                               AAB80884;
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                                                                                                                                                                                                                                                                                   immunoglobulin
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                                                                                                                                                                                                                                                                                          Anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                                   gamma
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08-FEB-1991;
10-FEB-1992;
08-DEC-1992;
                                                                                   07-JUN-1995;
                                                                                                      13-FEB-2001.
                   (PROG-)
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                    PROGENICS
Beaudry
                                       91US-00653684.
92WO-US001143.
92US-00960440.
                                                                                  95US-00485372
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Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ or treating a subject having CD4+ cells infected with HIV involves CD4-IgG2 chimeric heterotetramer to form a complex with the HIV.

using

Disclosure; Fig 4; 55pp; English

N-PSDB;

2001-264981/27 DB; AAF77830.

The present invention relates to a method for inhibiting infection of a CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2 chimeric heterotetramer to form a complex with the HIV (CD4 = cluster of differentiation 4; IgG2 = immunoglobulin gamma 2). CD4 is a cell surface glycoprotein that is expressed primarily on the surface of T cells. In man, CD4 is the target of interaction with HIV. The heterotetramer has

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                             Protein
                                                                                                                                                         Synthetic.
                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                 mutant; mutein.
                                                                                                                                                                                                                                                                                                           CD4-immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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1. .25
/label= Signal_peptide
26. .530
/note= "Mature CD4-IgG
                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                            G2;
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                                                                                                                                                                                                                                                                                                           (IgG2)
  "Mature CD4-IgG2 chimeric heterotetramer"
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Pred. No. 8.9e-108;
                                                                                                                                                                                                                                                                                                              chimeric heterotetramer.
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Best Local Similarity
Matches 409; Conserv
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10-FEB-1992;
08-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a purified CD4-immunoglobulin (Ig)G2 chimeric heterotetramer (I) that neutralises human immunodeficiency virus-1 (HIV-1) having two heavy chains encoded by an expression vector designated CD4-IgGENCPARCEMV. (I) and a composition (II) comprising (I) or designated CD4-kLC-pRcCMV. (I) and a composition (II) comprising (I) or (I) linked to a toxin, are useful for inhibiting HIV infection of a CD4 cell, and preventing a subject being infected with HIV by blocking the spread of HIV infection. This is the amino acid sequence of the CD4-immunoglobulin G2 chimeric heavy chain chimeric heterotetramer useful in this is the control of the control
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVEGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                  TVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNW
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KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                        YVDGVEYHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTIS
                                                                                                         YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                  ----KSCDKTHTCP-BLLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                                                                                                                                                                         VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDK
                                                                                                                                                                                                                                                                                                                                                                                          TWTCTVLQNQKKVEFKIDIVVLAFASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP
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92WO-US001143.
92US-00960440.
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77.3%;
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Pred. No. 8.9e-108;
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KTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPM

382 420 322 300

207 240

360 262 207

180 180 120

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RESULT 20
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                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel nucleic acid (I) encoding a fusion protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II) and a DNA sequence encoding amino acids 1-173 of CD4 (II) and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light chain (III). The products pf the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding to gpl20. The fusion protein is useful for treating human immunodeficiency virus (HIV) or similar immunodeficiency virus (SIV). This sequence represents the fusion protein CD4Bgammal which is constructed from CD4 linked to human IgG1 upstream of the hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JAN-1988;
23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Col 59-70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusion protein; human; CD4; IgG1; immunoglobulin; gp120; anti-human immunodeficiency virus; CD4Bgamma1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
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                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                             MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                             MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                               ILGNQGSFLTKGPSKLNDRADSRRSLWDQCNFPLIIKNLKIEDSDTYICEVBDQKBEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     616 AA;
TWTCTVLQNQKKVEFKIDIV--
                                              LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                              ILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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89US-00299596.
92US-00896781.
93US-00057952.
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                                                                                                                                                                                                                                                                                                                                     Score 2081; pr
Pred. No. 1.8e-
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                e 2081; DB 3;
. No. 1.8e-107;
[smatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                            Length 616;
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N-PSDB; AAZ48205.
                                                                                                                          Seed
                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                             HIV; extracellular; CD4; gp120; immunoglobulin; secreted protein; SIV infection; medicament.
                                                                       the
                                                                             New fusion
                                                                                                                                                             20-JAN-1989;
                                                                                                                                                                              20-JAN-1989;
                                                                                                                                                                                                14-SEP-1999.
                                                                                                                                                                                                                CA1340741-C.
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                                                                                                                                           (GEHO ) GEN
                                                                   fusion gene encoding immunoglobulin-CD4 fusion proteins, uses treatment of HIV or simian immunodeficiency virus infections
                                                                                                                                                                                                                                  sapiens
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                                                                                                                                                                                                                                                                                        fusion
                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                    LHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEAPELLGGPSVFLFPPKPKDTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
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                                                                                                                                                                                                                                                                                                                                                                                          LHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                            FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
                                                                                                                                           HOSPITAL
                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                             89CA-00588749
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                                                                                                                                                                                                                                                                                                                                             protein;
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                                                                                                                                                                                                                                                                      fusion
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                                                                                                                                                                                                                                                                      protein;
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The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gpl20 when fused to an immunoglobulin (Ig) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes

Example 1;

Page 61-68;

89pp; English

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Matches 419
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Fusion protein; diagnosis; CD4;
                                                                                                                                                                                                                        25-MAR-2003
02-NOV-1992
                                                                                                                                                 Genetic
                                                                                                                                                                                                                                                                                                                                 AAP93008
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                                                                                                            site upstream
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                        construct which encodes stream of the CH1 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEAPELLGGPSVFLFPPKPKDTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWTCTVLQNQKKVEFKIDIV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVFGLTANSDTHLLOGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                    (revised)
(first entry)
immunoglobulin-like molecule; HIV; SIV; therapy;
gp120; binding fragment; glycoprotein; variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.0%;
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; Pred. No. 1.8e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                    729
                                                                                                            CD4 linked to human IgG1 at the (fusion protein CD4H-gamma-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
L.8e-107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PELLGGPSVFLFPPKPKDTL
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LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEASTKGPSVFPLAPSSKSTSGG

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LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                   plasmid which encodes an antibody in which the variable region of the gene has been deleted (see wO87-02671). The CD4 portion of the figure and the membrane spanning domain, or the extracellular region and the membrane spanning domain, or the extracellular region and is pref. from IgM, IgCl or IgG3. The following are specifically claimed: fusion proteins CD4H-gamma-1, CD4Mmu, CD4Pmu, CD4E-gamma1, and CD4Mmu (No.67608), pCD4P-gamma (No.67609) and pCD4E-gamma-1 (NC1061/P3) at the ATCC under accession number 67611. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                            Sequence 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Table 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin-CD4 fusion proteins - used for
infections or detecting HIV or SIV in sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEHO)
                                                                               181
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                                                                                                         121
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                                                                                                                                                                                                                                                                        428;
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                                                                                                                        LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNLQGGKTLSVSQLELQDSG
                                                                                                        LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                            ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                  MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                      TWTCTVLQNQKKVEFKIDIV----------
                                                                                                                                                              ILGNQGSFLTKGPSKINDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                    TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                   77.0%;
                                                                                                                                                                                                                                                                      <u>,</u>
                                                                                                                                                                                                                                                                      Score 2079.5; DB 1;
Pred. No. 2.5e-107;
0; Mismatches 3;
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
04-FEB-1994;
The present sequence is that of fusion protein CD4Hgammal comprising textracellular portion of CD4, which binds to HIV gpl20, linked at its terminus to the human IgG1 heavy chain. To obtain the fusion protein, encoding CD4 was linked to IgG1 DNA at the Hind3 site upstream of the region (see AAA50660). Fusion protein CD4Hgammal and a nucleic acid encoding it are claimed. Also claimed are a vector comprising the nucl
                                                                                                                                                                                   CD4-immunoglobulin SIV.
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Pred. No. 2.5e-107;
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14-MAR-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gp120 when fused to an immunoglobulin (1g) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gp120 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be used for treating HIV or SIV infections in animals, can be used for treating HIV or SIV infections in enimals. The present sequence represents the fusion protein CD4Hgammal where the CD4 is linked to human IgG1 at the Hind3 site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 729 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful the treatment of HIV or simian immunodeficiency virus infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 25-36; 89pp; English
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428; Conserv
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LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                      TWTCTVLQNQKKVEFKIDIV-----
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                                                                                                                                                                                                    TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                  QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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ilarity 58.8%;
Conservative
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WPI; 1994-065392/08. N-PSDB; AAQ55751.

GP,

Maddon

PROGENICS PHARM

07-AUG-1992; 06-AUG-1993;

92US-00927931 93WO-US007422 Region

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CH2 Region

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CH3 Region

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                                                                                                                            YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA
                                                                                                                                                                                  VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
                                                                                                                                                                                                                                                                                                                                 LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEASTKGPSVFPLAPSSKSTSGG
KSLSLSPG 728
                                                                      VEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
                                                                                                           YKCKVSNKALPAPIEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA
                                                                                                                                                                                                                      ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE
                                                                                                                                                                                                                                     ------EPKSCDKTHTC----PELLGGPSVFLFPPKFKDTLMISRTPE
                                                                                                                                                                                                                                                                            TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
                         KSLSLSPG 431
                                                     VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
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RESULT 25
AAR46679
ID AAR46
CD4; gamma; heavy chain; chimeric; chimaeric; immunoconjugate; HIV; human immunodeficiency virus; radionuclide; toxin; therapy; treatment;
                                                                                                                                                                                                                                                25-MAR-2003
08-AUG-1994
                                                                                                                                                                                                                                                                                AAR46679 standard;
                                                                                                                                           Region
                                                                                                                                                                      Region
                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                  CD4-IgG2 chimeric heavy chain.
                                                                                                                                                                                                                                                                    AAR46679;
                                                                                                                                                        Region
                                                                                                                                                                                                       imaging;
                                                                                                                                                                                                      detection; targetting; immunoglobulin; IgG
                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                         l. .203
/label= CD4 Region.
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                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                protein; 530 AA
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el= CH1 Region.
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RESULT 26
AAY51078
ID AAY51
XX
AC AAY51
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DT 23-MA
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DT 23-MA
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DE Humar
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KW Fuelc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A tetramer comprising 2 IgG2 heavy chains or two CD4-IgG2 chimeric heavy chains and two kappa light chains or CD4-kappa light chains (AAR4680) linked to a non-peptidyl toxin or a gamma radiation-emitting radionuclide of low to moderate cytotoxicity. The resulting immunoconjugate comprising the toxin can be used to kill HIV infected cells and to treat HIV infected to toxin can be used to kill HIV infected cells in the comprision of the comprision of the comprision of the comprision of the comprision of the comprision of the comprision of the comprision of the radionuclide can be used to image HIV infected tissue, to calculate the stage of HIV infection or the efficacy of an anti-HIV treatment using the imaging technique and for determining the prognosis of an HIV infected subject. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2 immuno:conjugates - used to kill HIV-infected cells and to image stage HIV infection.
Fusion protein; human; CD4; IgG1; immunoglobulin; anti-human immunodeficiency virus; CD4H-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                             Human
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                                           fusion
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                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
                                                                                                                                                                                                                                                                                                                              YVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKQXKCKVSNKGLPAPIEKTIS
                                                                                                                                                                                                                                                                                                                                              YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
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                                                                                                                                                                                                             LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TWTCTVLQNQKKVEFKIDIVVLAFASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP
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                                           protein
                                                                         (first
                                                                                                                                  protein; 729
                                                                         entry)
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76.7%;
                                           CD4H-1
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Pred. No. 3.2e-107;
2; Mismatches 13;
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             gp120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JAN-1988;
23-JAN-1989;
09-JUN-1992;
12-APR-1993;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Col 15-30; 39pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusion protein useful for the treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                     LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEASTKGPSVFPLAPSSKSTSGG
                                                                                                                 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                                                             TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
                                                                                -----PC-----
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89US-00299596.
92US-00896781.
93US-00057952.
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58.7%;
PAP--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2069.5; DB 3;
Pred. No. 9.1e-107;
0; Mismatches 4;
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of CD4
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virus

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RESULT :
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                         The fusion protein genes of the invention pref. comprises cDNA sequences which encode CD4 or a fragment which binds gp120 ligated to an expression plasmid which encodes an antibody in which the variable region of the gene gene has been deleted (see Wo87-02671). The CD4 portion of the fusion protein may comprise the complete CD4 sequence, the 370 AA extracellular region and the membrane spanning domain, or the extracellular region. The greatly claimed: from IgM, IgG1 or IgG3. The following are specifically claimed: fusion proteins CD4Hlambda1, CD4Hmu, CD4Pmu, CD4Elambda1, and CD4Mmu (No. 67608), pCD4Plambda (No. 67609) and pCD4Elambda1 (No. 67610). (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion protein;
diagnosis; CD4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetic construct which encodes CD4 linked to human IgG1 at the downstream from the hinge region (fusion protein CD4Blambda1).
                                                                                                                                                                                                                                                              WPI; 1989-214472/30.
N-PSDB; AAN90360.
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03-AUG-1992
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                                                                                                                                                                                      Example; Table 5, Page 48-55; 68pp; English.
                                                                                                                                                                                                                   infections or detecting
                                                                                                                                                                                                                    Immunoglobulin-CD4 fusion proteins - used for treating
infections or detecting HIV or SIV in sample.
                                                                                                                                                                                                                                                                                                                                                                  22-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                             20-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-1989
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gp120; binding fragment; glycoprotein; variable region
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Query Match

76.1%;

Score 2056;

ВB 1;

Length 614;

12-SEP-2000

Sequence 614

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Matches 416; Conservative
                                                                                           Key
Protein
                                                                                                                                                                                                            09-JAN-2001
                                                                                                                                                   gp120;
                                                                                                                                                               CD4; IgG1; human; CD4Bgamma1; fusion
                                                                                                                                                                                     CD4-IgG1 fusion protein CH4Bgamma1.
                                                                                                                                                                                                                                  AAB19511;
                                    US6117656-A
                                                                     Protein
                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                          FYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 416
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                                                                                                                                                                                                            (first
                                                                                                                                                   diagnosis
                                                                    /note= "CD4 extracellular region"
400. .616
                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                            entry)
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1; Mismatches 12;
                                                                                                                                                                                                                                                         616
                                                                                                                                                              protein; immunoglobulin; HIV; SIV;
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Best Local :
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
04-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of fusion protein CD4Bgammal comprising the extracellular portion of CD4, which binds to HIV gp120, linked at its C-terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA encoding CD4 was linked to IgG1 DNA at the Ban1 site downstream of the hinge region (see AAA50664). Fusion protein CD4Bgammal and a nucleic acid encoding it are claimed. Also claimed are a vector comprising the nucleic acid, and a method of producing the fusion protein in secreted form using a transformed host cell. The fusion protein may further comprise a therapeutic agent, radiolabel or NMR imaging agent. The fusion protein can be administered to an animal (including humans) for treatment of HIV or SIV infection, and can also be used in assays for HIV or SIV, imaging and tissue stains. IgG1 fusion proteins such as CD4Bgammal provide both complement-mediated and cell-mediated immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 616 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD4-immunoglobulin fusion
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                                                                                                                                                                                                                                                                                                                                                                         LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                                                                                                                                                                                                                                                                                                         ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
 DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKG
                                                MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ
                                                                                          LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEAPELLGGPSVFLFPPKPKDTL
                                                                                                                                                       LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                   QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                                                                                              TWTCTVLONOKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTCSGELWW
                                                                                                                                                                                                                                                                                                               LVFCLTANSDTHLLQGQSLTLTLESPPCSSPSVQCRSPRCKNIQCCKTLSVSQLELQDSC
                              MISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRYVSVLTVLHQ
                                                                                                                                                                                                                                                                                                                                                                                                         ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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89US-00299596.

92US-00896781.

93US-00057952.

94US-00191708.
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66.8%;
                                                                                                                                                                                    ----SCDKTHTC----
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                                                                                                                                                                                                                                                   -----APEPK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1999; DB 3;
Pred. No. 6.2e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                       -----PELLGGPSVFLFPPKPKDTL
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                                                    protein, e.g. the present sequence, linked to a targetting polypeptide chat binds a molecule, which differentiates a host cell from a tissue graft cell, or selectively targets a stimulator cell involved in the cautoimmune response. A veto molecule, in which the protein binds a molecule that targets stimulator cells, can be used to suppress an immune cresponse and therefore treat autoimmune diseases, e.g. systemic lupus crythematosus, myasthenia gravis, rheumatoid arthritis, insulin dependent diabetes mellitus, multiple sclerosis, coeliac disease, autoimmune thyroiditis, Addison's or Grave's diseases and rheumatoid carditis, allergies and other immunological diseases and rheumatoid carditis, allergies and other immunological diseases and rheumatoid carditis, combined that differentiates graft and host cells, the veto molecule can be used to reduce transplant rejection. The veto molecule provides specific regulation of particular stimulator cells that can kill graft cells or respond to autoantigens, but leave other stimulator cells can kill graft cells or respond to autoantigens, but leave other stimulator cells can kill graft cells or or CDB positive cells can be regulated without one affecting the other. The veto molecule can be administered locally to minimise generalised immunosuppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tlymphocyte veto molecule comprising response cell activating protein linked to molecule that targets stimulator cell marker, used for selective suppression of immune response, e.g. prevention of graft rejection or treatment of auto-immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          targetting polypeptide; suppression; immune response; treatment; autoimmune disease; allergy; immunological disorder; fusion protein; immunoglobuin G2a; transplant rejection; constant region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A novel T lymphocyte veto molecule is a chimeric molecule comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 40; Page 75-76; 309pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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                          N-PSDB;
                                                     WPI; 1992-056814/07
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05-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR20634 standard; protein;
                                                                                                                                                                                                                                                                                        11-JUL-1990;
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91US-00665218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V1V2-hCH2-KA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= hinge
229. .343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= V1V2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= signal_cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.8%;
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1; Mismatches 51;
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Nucleic acid sequences for production of CD4 chimeric protein - used transfect streptomyces, contg. LTI signal sequence linked to pro-pept sequence facilitating peptide cleavage. in - used to pro-peptide

23; 47pp; English

The sequence was deduced by sequencing the plasmid vector VIV2-hCH2- KA CC in S. lividans strain 1326. The protein has domains contg. peptides of CC different function. It contains a CD4 chimera (VIV2) in which the carboxy terminal portion of the protein consists of a murine immunoglobulin light chain constant region, linked to the signal peptide of Streptomyces LTI, CC modified at its N-terminus to include Lys-Arg. Also included is the IgG1 constant region comprising the hinge and CH2 motifs. Human IgG1 is the CC constant region comprising the hinge and CH2 motifs. Human IgG1 is the CC complement and ADCC. The CD4 chimeric proteins may be expressed in CC complement and ADCC. The CD4 chimeric proteins may be expressed in CC complement, and the LTI CD4 protein increases the stability of the CD4, CC thus increasing the serum half life and/or potency against HIV infection CC and inhibit virus-induced cell fusion, relative to soluble CD4. By CC altering only one amino acid at position 2 near the N terminal of CD4 (VI region) from Lys to Ala, a heterologous protein is expressed which is CC efficiently secreted and correctly processed to remove the entire LTI CC signal sequence, but which still retains the gpl20 binding capacity. By modifying the pro-peptide you avoid deleterious effects of additional CC amino acids on the function of the protein. See also AAR20635,6

343 AA;

Ś 밁 δ B á 밁 á 밁 Query Match
Best Local Similarity
Matches 300; Conserv 322 309 142 139 202 199 82 19 79 22 LTGAALAKAVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLND LTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKID RADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQS LPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLND SNKALPAPIEKTISKAKGOPRE 330 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV RADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQS SNKALPAPIEKTISKAKGOPRE 343 VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV IV-----PCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKFKDTLMISRTPEVTCVV LTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKID IVVLAFQKASKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDT Conservative 57.2**%**; 0, Score 1546; DB 2; Pred. No. 4.5e-78; 0; Mismatches 12 2 Indels Length 343; LMISRTPEVTCVV 10; Gaps 308 248 141 18 261 201

AAR89441 standard; peptide; 254 ₽

26-SEP-1996 (first entry)

IgG1 hinge, CH2 and CH3 domains.

RESULT 31
AAR89441
ID AAR89
AC AAR89
AC AAR89
AC AAR89
AC AGAR8
XX
XX
DT 26-S1
XX
CD7;
KW CD7;
KW CD7;
KW humaai
KW dend:
XX
XX
Homo CD7; transmembrane domain; chimeric receptor; human; CD4; HIV; proteinaceous alpha-helix; T dendritic cell; therapy; mammal; infection. CD5; CD34; CH2; CH3; IgG1; cell; B cell; neutrophil;

Homo sapiens

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RESULT 32
AAR78667
ID AAR78
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AC AAR76
AC AAR76
DT 11-AE
XX
XX
XX
DT 11-AE
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the human IgG1 hinge, CH2 and CH3 domains. This sequence is included in the membrane bound proteinaceous chimeric receptor of the invention. Alternatively the transmembrane region of the chimeric receptor contains a portion of the CD7, CD5 or CD34 transmembrane domains. The extracellular portion of the chimeric receptor contains a fragment of CD4 (amino acids 1-394 or 1-200 of the CD4 sequence) which specifically recognises and binds HIV-infected cells, but does not mediate HIV infection. The extracellular domain of the receptor is separated from the cell membrane by 48 or 72 angstroms, or by one or more proteinaceous alpha-helices. The cells expressing the receptor are preferably T cells, B cells, neutrophils, or dendritic cells. The therapeutic cells expressing the chimeric receptor are administered to a
             IgG1 hinge,
                                         11-APR-1996 (first entry)
                                                                                                 AAR78667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Fig 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Membrane-bound chimeric receptor comprising extracellular portion including CD4 fragment : cells expressing receptor can be used for treatment of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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24-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                        NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                              PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAE 440
                                                                                                                                                                                                                                                                                                   I SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                         NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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                                                                                                                                                                      AQDGELDGLWTTDP
                                                                                                                                                                                                  ACCELLCLWITTOP
                                                                                                                                                                                                                      ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treat HIV infection
              CH2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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95US-00394388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134pp; English.
                                                                                               protein; 254
              CH3 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Romeo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1338.5; DB 2;
Pred. No. 1.1e-66;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kolanus
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RESULT 33
ADD13790
ID ADD13
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AC ADD13
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AC ADD13
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DT 01-JA
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DE Plasm
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KW 11bra
KW T cel
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 248; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human IgG1 hinge, CH2 and CH3 domains (AAR78668) are used in the construction of a chimeric receptor utilised in the targeted cytolysis HIV-infected cells. The chimeric receptor comprises the extracellular domain (pref. amino acids 1-394 or 1-200) of CD4 linked via the CD7 transmembrane domain to an intracellular portion, e.g. of T-cell recept protein zeta. The IgG1 portion of the chimeric receptor is encoded by t DNA sequence given in AAQ96101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Fig 25; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric receptor; CD4; T-cell receptor; HIV; cytolysis; human immunodeficiency virus; adoptive immunotherapy; IgG1.
                                                                                                                ADD13790 standard; protein; 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-FEB-1994;
02-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                        206 EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytolysis of HIV-infected
                                                                                                                                                                                                                                                PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAE
                                                                                                                                                                                                                                                                                                   ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                    NWYVDGVEVHNAKTKPRBEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                        AQDGELDGLWTTDP 454
                                                                                                                                                                                                                                  PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAE
                                                                                                                                                                                                                                                                                   ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                      NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSKKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                        EPKSCOKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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94US-00284391.
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97.6%;
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                                                                                                                                                                                254
                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1332.5; DB
Pred. No. 2.3e-66;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cells -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD4 receptor-bearing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254;
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of.

library; transfection; humanized T cell receptor; circular.

Plasmid

pBS

(first entry)

loxP-IgG1/pBS loxP-IgG1delta350/pBS loxPIgGdeltaCH1

protein

monoclonal antibody; antigen,

ADD13790

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                                                                                                                                                     This invention describes a novel method of preparing a library of protein CC -producing eukaryotic cells comprising (a) introducing specific ce combination signals into one or two chromosomal gene loci. (b) CC Expanding at least one of the modified cells, (c) Transfecting many CC different DNA sequences, each flanked by recombination signals, into the expanded cells and (d) Integrating the DNA sequences into the gene loci on the basis of the recombination signals and the appropriate CC recombinase. The resulting cells express different proteins, each from an integrated DNA sequence and the proteins are bound to the cell surface. The method is particularly used to produce libraries of humanized CC monoclonal antipodies, for selection of those with affinity for particular antigens and useful for diagnostic or therapeutic use. CLibraries of high diversity, provides easy, quick and automatable selection from a large number of proteins, allows relatively simple CC selection from a large number of proteins, allows relatively simple calteration of the expressed gene (e.g. fusion to other protein-coding cs simple verification and characterization of selected cell lines. The method does not require incorporation of a resistance marker. This sequence represents the construct DSS loxP-IgGlDeS loxP-IgGldeIta350/pBS
                                                                                         Query Match
Best Local Similarity
Matches 266; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparing library of protein-producing eukaryotic cells, useful for producing humanized high-affinity antibodies, comprises introducing specific recombination signals into chromosomal gene loci and integrating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2001; 2001EP-00123596
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Homo sapiens
                                                                                                                                                     Sequence
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                                                                                                                                                                                   loxPIgGdeltaCH1 described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                variety of
   181
                                                             151
                             S
                                                                                                                                                     400 AA;
                                                             PSVQCRSPRGKNIQGG-----
                             PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moldenhauer G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note= "Murine IgG2 M2'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note=
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 ----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC----PELLG
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                                                                                                       49.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "human IgG1 CH2"
                                                                                           8
                                                                                        Score 1327.5; DB 7;
Pred. No. 7.1e-66;
8; Mismatches 22;
                                                                                                                                                                                   the disclosure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Poustka
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                                                             --KTLSVS----
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                                                          -----OLELQDSG----
                                                                                                                       Length
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   221
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RESULT 34
ADD13781
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33
                                     Preparing library of protein-producing eukaryotic cells, useful for producing humanized high-affinity antibodies, comprises introducing specific recombination signals into chromosomal gene loci and integrating
                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                                                                                   T cell receptor; circular.
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                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid pBS MbIgG1M/ pBS MhIgG1Mdelta250 protein
                                                                                  N-PSDB;
                                                                                                                                                                                                                       EP1298207-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                             library; transfection; humanized monoclonal antibody; antigen;
                                                                                                                                     (DEKR-) DEUT
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                                                                                  2003-383833/37.
DB; ADD13780.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WQQGNVFSCSVMHEALHNHYTQKSLSLSP--GLQLDETCAEAQDGELDGLWTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
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                             of DNA sequences
                                                                                                                                     KREBSFORSCHUNGSZENTRUM
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                                                                                                                Moldenhauer
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98. .112
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1. .97
                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                         /note= "murine IgG1 M2'
                                                                                                                                                                                                                                                                                                      /note= "human IgG1 CH2"
                                                                                                                                                                                                                                                               'note=
                                                                                                                                                                                                                                                                                    'note=
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                                                                                                                                                                                                                                                                "murine
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                                                                                                                Kuehlwein
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Example 1;

Fig 12B; 75pp; German

variety

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ABJ37104
ABJ37107
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AC ABJ3
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COnc
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Best Local
                                                                                                                                                                                                              antiarthritic;
dimeric protein
                                                                                                                                                                                                                                                                        Antiinflammatory; antibacterial; immunosuppressive; antirheumatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABJ37104 standard;
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                                                             WO2003010202-A1.
                                                                                                                                                                                       rheumatoid arthritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WQQGNVFSCSVMHEALHNHYTQKSL-SLSP--GLQLDETCAEAQDGELDGLWTT
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                                                                                                                                                                                       cachexia; inflammation;
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                                                                                                                                                                                                                                                                                                                                         human
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                                                                                                                                                                                                                                              domain;
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AAR42162 ID AAR XX

AAR42162 standard; protein;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New concatameric protein having two soluble domains, useful for diagnosing and treating disorders associated with the dimeric protein its glycosylated form, such as inflammation, septicemia, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 156-158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arthritis and cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-2002; 2002WO-KR001427
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                                                                      GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
                                                                                                       DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
                                                                                                                                                                                                                  SSVEPVSCPA-EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV
                                                                                                                                                                                                                                FKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV
                                                                                                                                                                                                                                                                                                  LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWT-----CTVLQNQKKVE
                                                                                                                                                                                                                                                                                                                           KIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLK-----IQERVSKPKISWTCINTTLT
                                                                                                                                                                                                                                                                                                                                                                                  DDIKWEKTSDKKKIAQFRKEKE----TFKEKDTYKLFK----
                                                                                                                                                                                                                                                                                                                                                                                                            DTVELTCTASOKKS1OFHWKNSNOIKILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPL
က္က:
                                                    GOPENNY
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                         431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1287.5; DB 6;
Pred. No. 1.3e-63;
2; Mismatches 62;
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Best Local (
                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV-neutralising monoclonal antibody; immunoglacquired immune deficiency syndrome; chimeric surface glycoprotein gp120; V3 loop.
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant human antibody - with HIV neutralising activity against at least two isolates, useful for preventing or treating infection in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Emini EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9319785-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody; HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
27-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR42162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 9; Fig 2A; 154pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1993-336600/42.
 265
                                                                                         180
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                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ49834.
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                              CDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                                                         GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKS
                                                                                                                                                      VWGKGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
                                                                                                                                                                                                                   TISRDDSKNTLYLOMN-----SLKTEDTAVYSCTTDG----FIMIRGVSEDYYYYYMD
                                                                                                                                                                                                                                                                                                            LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLND------
                                                                                                                                                                                                                                                                                                                                                                                                     461 AA;
                              CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                                                                                        ----QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKS
                                                                                                                                                                                     --GQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----
                                                                                                                                                                                                                                                ---RADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ 135
                                                                                                                                                                                                                                                                               LVKPGGSLRLTCVASGFTFSDVWLNWVRQAPGKGLEWVGRIKSRTDGGTTDYAASVKGRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conley AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombinant antibody 447-52D heavy
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
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                                                                                                                                                                                                                                                                                                                                          Score 1287; DB 2;
Pred. No. 1.5e-63;
0; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnson LS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfarr
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                                                                                                                                                                                                                                                                                                                                                                     Length 461;
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                                                                                                                                                                                                                                                                                                                                          82;
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RESULT 37
AAO18400
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XX AAO18
XX AAO18
XX AAO18
XX Matur
XX Mose
KW Neopl
XX Mose
KW Neopl
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YX 12-0(
YX 11-0(
YX 11
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Best Local
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to humanised anti-lymphotoxin beta receptor (LT-beta-R) antibodies. These are derived from the murine LT-beta-R binding antibody CBE11 and can be used to treat neoplasia in humans. The present sequence is a humanised murine CBE11 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New humanized anti-lymphotoxin-beta receptor antibody, useful for treating or reducing the advancement, severity or effects of neoplasia, particularly solid tumors (i.e. carcinomas) including colorectal cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-OCT-2000; 2000US-0240285P
13-MAR-2001; 2001US-0275289P
21-JUN-2001; 2001US-0299987P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-583337/62.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse; humanised antibody; lymphotoxin beta receptor;
neoplasia; LT-beta-R; light chain; heavy chain; varial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mature humanised murine CBE11 heavy chain variable domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Page 25-26; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-2001; 2001WO-US032140
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                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                   275;
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                                                                                                                                                                                                                                                                                    30 LGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKILGNQGSFLTKGPSKLN----
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                                                      -GOSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----
                                                                                                                                                                      -DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
WGOGTTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG
                                                                                                                                                                                                                                LVKPGGSLRLSCAASGFTFSDYYMYWFRQAPGKGLEWVATISDGGSY-TYYPDSVKGRFT
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                                                                                                             ISRDNAKNSLY-----LOMSSLRAEDTAVYYCAREE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer.
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                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                               47.6%;
                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                               Score 1285.5; DB 5; Pred. No. 1.7e-63;
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                                                                                                                                                                                                                                                                                                                                                      Mismatches
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variable region.
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                                                                                                                   ---NGNFYYFDY 109
                                                                                                                                                                                                                                                                                                                                                                                                                449;
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RESULT 38
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Query Match 47.5%; Score 1284.5; D
Best Local Similarity 59.4%; Pred. No. 2e-63;
Matches 280; Conservative 30; Mismatches
                                                       Polynucleotides encoding the L and H chains of human anti-HBs Ab are given in AAQ49943-Q49944. The Ab can be easily produced in large quantities for therapeutic use. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                       Human anti-hepatitis B surface antigen antibody gene - can produce L and H chains of the antibody in large quantity.
                                                                                                                                                    WPI; 1993-336913/42.
N-PSDB; AAQ49944.
                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
29-APR-1994
                                     Sequence
                                                                                                      Disclosure;
                                                                                                                                                                                                                     30-MAR-1992;
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                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                           Antibody; Ab;
                                                                                                                                                                                                                                                                                                                                                                                             Human anti-HBs heavy chain
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                                                                                                                                                                                                   (SUNR ) SUNTORY LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSC
                                                                                                    Fig 6-8; 46pp; Japanese.
                                                                                                                                                                               Matsukura
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                         light; heavy; chain; hepatitis B; HB; surface antigen
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10. .459
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/label=
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                DB 2;
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Indels
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                Length 459;
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            PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                      ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 380
                                                                               EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                              ------QLELQDSG-------TWTCTVLQNQKKVEFKIDIVPCPAP 205
                                                                                                                                                                                                        HRFDSWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSG 173
                                                                                                                                                                                                                                                                                        GGGVV--QPGRSLRLSCAASGFTFSSNSMHWVRQAPGKGLEWVAVILYDGNHKFYADSVK 74
                                                                                                                                                                                                                                                                                                   GNKVVLGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKIL---GNQGSFL--TK
                                                                                                                                                                                                                            HLLQ--GOSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS---- 172
                                                                                                                                                                                                                                               GPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                    431
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RESULT 39
AAW05829
B-cell lymphoma; humanised antibody; bispecific
                                                                                                                               Key
                                           Domair
                                                        Domain
                                                                                 Region
                                                                                              Region
                                                                                                           Region
                                                                                                                                                   Mus sp.
                                                                                                                                                        Homo; sapiens
                                                                                                                                                                                                      16-OCT-2003
27-JAN-1997
                                                                                                                                                                                                                          AAW05829;
                                                                                                                                                                                                                                       AAW05829
           WO9626964-A1
                                                                     Domain
                                                                                                                         Domain
                                                                                                                                            Chimeric.
                                                                                                                                                                     leukaemia; hybridoma; monoclonal antibody.
                                                                                                                                                                                         Humanised 1D10 antibody heavy chain.
                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                      (revised)
(first entry)
                                                      /117. .214
/label= CH1
215. .220
                                   215. .229
/label= Hinge
230. .339
/label= CH2
                        340. .446
/label= CH
                                                                                                           /label= Variable_domain
31. .35
                                                                                                                               Location/Qualifiers
                                                                                        label= CDR2
                                                                                              'label= CDR1
50. .65
                                                                           label= CDR3
                                                                                                                                                                                                                                     protein;
                                                                                 .105
                        CH3
                                                                                                                                                                                                                                       446
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                                                                                                                                                                           antibody; myeloma;
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06-SEP-1996.

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Best Local S
Matches 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variable region framework and complementarity determining regions from the murine 1D10 antibody specific for a 28/32 kDa antigen found on the surface of malignant B-cells. It can be coexpressed with humanised 1D10 light chain (see also AAW05828) in mammalian host cells. Bispecific antibodies can be constructed that include a first binding fragment comprising humanised M291 heavy and light chain variable regions (see also AAW05826, AAW05830), and a second binding fragment comprising humanised 1D10 heavy and light chain variable regions. Such antibodies are reactive with both T or NK cells and malignant B cells, and have therapeutic and diagnostic applns. (Updated on 16-OCT-2003 to standardis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New bi-specific antibody reactive with both T or NK cells and malignant B cells - also their humanised forms and hybridomas producing them, useful for treating or preventing leukaemia, lymphoma and myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapeutic
OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The humanised 1D10 antibody heavy chain (AAW05829) includes a var
region (see also AAW05823) consisting of human R3.5HG heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PROT-) PROTEIN DESIGN LABS INC. (IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS.
                                                                  348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Fig 4e; 85pp; English.
KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVKPSETLSLTCTVSGFSLTNYGVHWVRQSPGKGLEWIGVKWSGGSTEYNAAFISRLTIS
                                                                                    YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                           TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                                          CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                              ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                                            QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPP
                                                                                                                                                                                                                                                                                                           QDSG--------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC--
                                                                                                                                                                                                                                                                                                                                                VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHFTPAVL
                                                                                                                                                                                                                                                                                                                                                                               LESPPGSSPSVQCRSPRGKNIQGG------KTLSVS------QLEL
                                                                                                                                                                                                                                                                                                                                                                                                                   KDTSKNQVSLKLNSLTAADTAVYYC------ARNDRYAMDYWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   --WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTLT
                                                                     YTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gingrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Link BK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1282.5; DB 2;
Pred. No. 2.5e-63;
5; Mismatches 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variable
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RESULT 40 ABJ37106

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                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 272; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel concatameric protein comprising two soluble domains, in which an N-terminus of a soluble domain of a biologically active protein is linked to a C-terminus of an identical soluble domain or a different soluble domain of a biologically active protein. The methods and compositions of the present invention are useful for the diagnosis and treatment of disorders associated with dimeric protein or its glycosylated form, such as inflammation, septicaemia, cytotxicity, rheumatoid arthritis, cachexia and other inflammation-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New concatameric protein having two soluble domains, useful for diagnosing and treating disorders associated with the dimeric protein its glycosylated form, such as inflammation, septicemia, rheumatoid arthritis and cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiarthritic; immunomodulator; concatameric protein; sol
dimeric protein; inflammation; septicaemia; cytotoxicity;
rheumatoid arthritis; cachexia; inflammation; human.
                                                                                                                                                                                                                                                                                                                                               Sequence 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUL-2002; 2002WO-KR001427
                                                                                                                                                                                                                                                                                                                                                                                            related diseases. This sequence represents the human concatameric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MEDE-) MEDEXGEN
                                                                                                                                                                                                                                                                                                                                                                             the invention
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DB; ABT32049.
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       250
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                                                                                                                                                                                           IIKNLKIEDSDTYICEVEDOK-EEVOLLVFGLTANSDTHLLQGO---
                                                                                                                                                                                                                         DDIKWEKTSDKKKIAQFRKEKE------TFKEKDTYKLFK-----NGTL
DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVS
                                      SSVEPVSCPA-EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV
                                                                                                                                LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWT-----
                                                                                                                                                                KIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLK-----IQERVSKPKISWTCINTTLT
                                                                                                                                                                                                                                                        DTVELTCTASOKKSIOFHWKNSNOIKILGNOGSFLTKGPSKLNDRADSRRSLWDOGNFPL
                                                      FKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV
                                                                                                    CEVMNGTDPELNL-----YQDGKHLKLSQRVI--THKWTTSLSAKFKCTA-GNKVSKE
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                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibacterial; immunosuppressive; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee
                                                                                                                                                                                                                                                                                                 47.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choi
                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                   Score 1282.5; DB 6;
Pred. No. 3.5e-63;
2; Mismatches 63;
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                                                                                                                                                                                                                                                                                                                   Length
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Best Local S
Matches 272
                                                                                                                                                                                                                                      soluble domains, in which an N-terminus of a soluble domain of a biologically active protein is linked to a C-terminus of an identical soluble domain or a different soluble domain of a biologically active protein. The methods and compositions of the present invention are useful for the diagnosis and treatment of disorders associated with dimeric protein or its glycosylated form, such as inflammation, septicaemia, cytocoxicity, rheumatoid arthritis, cachexia and other inflammation-related diseases. This sequence represents the human concerning of the invariant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New concatameric protein having two soluble domains, useful for diagnosing and treating disorders associated with the dimeric protein its glycosylated form, such as inflammation, septicemia, rheumatoid
                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; Page 188-191; 211pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-2001; 2001KR-00045028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rheumatoid arthritis;
                                                                                          Local Similarity
les 272; Conser
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                                                           Claim
                                                                                  New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent
                                                                                                                                                                           30-SEP-1999; 99JP-00278291.
06-APR-2000; 2000JP-00105088.
                                                                                                                                          Hanai
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                                                           Page 175-179; 183pp; Japanese
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The present invention describes a monoclonal antibody which can reac specifically with ganglioside GD3. The antibody and its derivatives useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplifica of the invention

exemplification

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                                                                                                            /label= Mature_Hu266_heavy_chain
/note= "This sequence is specifically claimed
17"
                                                                                                                                                                                           /label= Signal_peptide
                                                                                                                                                                                                                                        Location/Qualifiers
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Pred. No. 3.5e-63;
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Best Local Similarity
Matches 282; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates a humanised antibody that specifically binds an epitope contained within positions 13-28 of amyloid beta peptide, Abeta. The antibody is useful to inhibit and reduce the formation of amyloid plaques or the effects of toxic soluble Abeta species in humans their fragments are used for the manufacture of a medicant. This includes the prolonged expression of recombinant sequences of them in human tissues for the treatment of clinical/pre-clinical Alzheimer's disease, Down's syndrome or pre clinical cerebral amyloid angiopathy. Specifically, the antibody is used to sequester Abeta into plasma, brain or cerebrospinal fluid to prevent/reverse accumulation of the Abeta peptide within the brain theraby improving cognition. The present sequence is the heavy chain of a humanised monoclonal antibody, Hu266, based on the mouse antibody 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-FEB-2000; 2000US-0184601P.
08-DEC-2000; 2000US-0254465P.
08-DEC-2000; 2000US-0254498P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 13; Fig 5; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New humanized antibody for the treatment of Alzheimer's comprises inhibition and reduction of the formation of amyloid plaques.
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NHYTQKSLSLSPG
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                                                                 PSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH
                                                                                          PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH
                                                                                                                                                     LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY
                                                                                                                                                                           LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY
                                                                                                                                                                                                                                          SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
                                                                                                                                                                                                                                                                                                                            CNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI
                                                                                                                                                                                                                                                                                                                                                                CTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMI
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tive 30; Mismatches
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A polypeptide (AAW11639) comprises a leader sequence, RF-1 heavy chain variable region (see also AAW11639), and human gamma 1 constant region. RF1 is a human monoclonal natibody (hMAb) specific for the fusion prott of respiratory syncytial virus (RSV). The polypeptide can be produced is eukaryotic host (e.g. CHO) cells transfected with vector NEOSPLA incorporating a DNA construct (AAT61241) including the RF-1 VH sequence
                                                                                                                                                                                        Human monoclonal antibody specific for respiratory protein - used for the prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monoclonal antibody; MAb; RF-1; RF-2; respiratory syncytial fusion protein; F-protein; vaccine; immunotherapy; therapy; Epstein Barr virus; immortalisation; recombinant antibody.
                                                                                                                                                   Example
                                                                                                                                                                                                                                                                                                                          Brams
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DB; AAT61241.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a new method of treating or preventing stroke and other neurological diseases in a human. The method involves administering a myelin-associated glycoprotein (MAG) antagonist or anti-MAG antibody, including altered antibodies or their functional fragment. The MAG antagonist or anti-MAG antibody, including altered antibodies or their functional fragment for their functional fragments are useful in preparing a medicament for treating or preventing stroke and other neurological diseases, or for inhibiting neurodegeneration and/or promoting functional recovery in a human patient suffering or at risk of developing stroke or other neurological disease, such as stroke, traumatic brain injury and spinal cord injury, chronic diseases including Alzheimer's disease, fronto-temporal dementias (tauopathies), peripheral neuropathy, Parkinson's disease, Huntington's disease and multiple sclerosis. The present amino acid sequence represents the mouse/human chimeric anti-MAG antibody heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating or preventing stroke and neurological diseases, e.g. Alzheimer's disease, multiple sclerosis or Parkinson's disease, comprises administring a myelin-associated glycoprotein (MAG) antagonist or anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 473 AA;
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                                                              GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
                                                                                                                            GOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                TKVD----KKVEPKSCDKTHTCPPCPAPELAGAPSVFLFPPKPKDTLMISRTPEVTCVVV
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Pred. No. 3.7e:
33; Mismatches
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3.7e-63;
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Query Match Best Local Similarity

47.48;

Score 1280; DB 2; Pred. No. 3.7e-63; 7; Mismatches 91

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Length 476; Indels

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                                                                     CC prostate adenocarcinoma. The invention encompasses 4B5 derivatives with CC immunologic specificity for antibodies specific for GD2. These CC derivatives, or antigen binding fragments, comprise regions of the 4B5 CC VDJ junction and regions spanning the 4B5 CDRs. Other derivatives include CC Fab, F(ab')2, Fab', scFv and isolated heavy and light chains (see also CAAM88465). Polynucleotide fragments (see AAX06951-54) encoding 4B5 CC antibody V regions are also provided, and therapeutic plasmids and CC polynucleotides. 4B5 has been shown to mimic GD2, and is particularly CC useful in generating a host immune response to cancer. Products of the CC invention can be used in the detection and treatment of e.g. astrocytoma, CC oligodendroglioma, ependymoma, meduloblastoma, primitive neural CC colorermal tumour (PNET), pancreatic ductal adenocarcinoma, small and CC large cell lung adenocarcinomas, squamous cell carcinoma, and liver metastases, CC hepatoma, cholangiocarcinoma, breast tumours such as ductal and lobular CC uterine and ovarian epithelial adenocarcinoma, and lobular cadenocarcinoma, squamous and adenocarcinoma, prostatic adenocarcinoma, couter and couter and couter and chronic leukemia, couter and chronic carcinoma, couter and chronic leukemia, couter and chronic leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibody 4B5 polynucleotides and polypeptides - used to develop products for the diagnosis and treatment of cancers and for prophylitherapy to reduce risk of recurrence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigen binding fragment 4B5; monoclonal antibody; cancer; neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma; sarcoma; lung carcinoma; metastasis; anti-idiotype antibody; GD2 antigen; hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW88464 standard; protein; 476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This polypeptide comprises the heavy chain variable region of the recombinant human monoclonal antibody (MAb) 4B5. 4B5 recognises antibodies specific for GD2 antigen antibodies. Antibodies specific for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 79-80; 83pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GD2 recognise various cancers including glioblastoma, neuroblastoma, malignant and/or metastatic melanoma, breast adenocarcinoma, lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAX06951
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DT 29-AU
CT 28-JU
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                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody; mAb; humanised; murine; mouse; 5c8; hu5c8; heavy chain; anti-CD145; CD145-antibody complex; 3D structure; three dimensional structure; drug design; drug discovery; activated T cell; CD40 interaction; T cell dependent immune response; agonist; antisponist; immune response; inflammatory response; autoimmune disease; altergy, inhibitor response; organ graft rejection; B cell cancer; Alzheimer's disease; multiple sclerosis; antiinflammatory; immunosuppressive; antiallergic; cytostatic, dermatological; antiasthmatic; nootropic; neuroprotective; antiarteriosclerotic; antiviral; antidiabetic; cardiant; antiischaemic; vasodilator; antibody; antiarteriosclerotic; antipsoriatic; immunomodulator; antibody;
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28-JUN-2002
Binding-site
                                                                                  Region
                                                                                                                                                                                                                            Homo sapiens
Chimeric.
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                                                                                                            "Forms
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Example 1; Fig 8; 470pp; English
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16-MAR-2001;
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                                                                                                                                             (BIOJ ) BIOGEN INC.
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                         stal comprising a CD154 polypeptide complexed with an anti-CD154 ibody, or its antigen binding fragment, useful for designing drugs i treatment of an autoimmune disease, an allergy, multiple sclerosis Alzheimer's disease.
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2001US-0276452P
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                                                                                                                    Taylor
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The invention relates to a crystal comprising a CD145 polypeptide in CC complex with an anti-CD45 antibody or its antigen-binding fragment, and CC the structure coordinates of such a crystal. In particular, the crystal CC comprises human CD145 (AAM49202) and a humanised version of the murine CC CD40L, gp39, T-BAM, 5c8 (hu5c8; AAM49203, AAM49204). CD145, also known as CC CD40L, gp39, T-BAM, 5c8 antigen, CD40CR and TRAP) is a 32 kD type II CC membrane glycoprotein which is translently expressed on activated T CC cells. It interacts with CD40 which is expressed on activated T CC cells. It interacts with CD40 which is expressed on activated endothelial CC cells. This CD40:CD145 interaction is required for T cell-dependent CC antibody responses, type I T-helper cell responses, and nittic oxide (NO) CC production by macrophages. NO mediates many of the pro-inflammatory CC activities of macrophages. No mediates many of the CD40:CD145 interaction CC via the use of an anti-CD145 antibody has been shown to reduce the CC symptoms of autoimmune and inflammatory conditions. The crystal structure of the invention can be used to determine the three dimensional structure of the CD145:anti-CD145 antibody complex, and thereby provide information about this interaction which may be of use in designing non-antibody CC CD145 agonists and antagonists which modulate the CD40:CD145 interaction. Such compounds may be used to a therapeutic agent, rejection of a CC allergy, an inhibitor response to a therapeutic agent, rejection of a CC allergy, an inhibitor response to a therapeutic agent, rejection of a CC allergy, an inhibitor response of a treatment of an unwanted to compense of a cell cancer. They may be specifically be used to creat systemic lupus erythematosus, lupus nephritis, benefitis, company restenosis, company restenosis, conschitis, emphysical conschitis, allone of the compense of the company of the provision of a complex conscribed by the company of the provision of a complex conscribed by the compense of the company of th nephropathy, glomerulonephritis, osteoarthritis, rheumatoid arthritis, psoriasis, atopic dermatitis, systemic sclerosis, radiation-induced fibrosis, Crohn's disease, ulcerative colitis, multiple myeloma and cachexia. Sequences AAM49203 and AAM49204 represent, respectively, heavy and light chains of the humanised version of the murine monoc

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RESULT 48
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Best Local S
Matches 275
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                                                                                                                                       Homo sapiens.
Chimeric.
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01-NOV-1999
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                      (BRIM ) BRISTOL-MYERS SQUIBB CO
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                                                                    99WO-US002949
                                                                                                                                                                                                                                                                                                                                   protein;
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Best Local Similarity
Matches 277; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents the heavy chain of a chimeric anti-CD40 antibody designated chi220. The antibodies are effective in modulating humoral immune response against T cell dependent antigens, collagen induced arthritis and transplant induced rejection. They are also useful for their anti-inflammatory properties. The antibodies have wide therapeutic applications, including autoimmune and inflammatory diseases and transplantation. The antibody can be used in a pharmaceutical composition for treating a patient suffering from a T cell mediated disorder. They can also be used to treat autoimmune diseases, inflammatory diseases, and transplantation. (Updated on 17-OCT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 452 AA;
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               FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                 HTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
                                                                                                                                                                                                                                                                                                     SLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS------
                                                                                                                                                                                                                                                                                                                                                                                       LKKPGETVRISCKAS---GYAFTTTGMQWVQEMPGKG---LKWIGWINTHSGVPKYVEDF
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FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                     REPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGS
                                                                   REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS
                                                                                                                                                                 HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
                                                                                                                                                                                                                                               -QLELQDSG-----TWTCTVLQNQKKVEFKIDIVFCPAPEPKSCDKT
                                                                                                                                                                                                                                                                           GTLVTVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT
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59.8%;
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Pred. No. 3.7e-63;
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ID AAY44
XX AAY44
XX AAY44
XX 25-AP
DT 25-AP
DE Human
XX Human
XX treat
XX treat
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Homo sapiens
                            Human; immune
                                                Human
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                                                                    25-APR-2000
                   treatment;
                                               immune
                                                                                                          standard;
                  prevention;
                                               system molecule,
                                                                   (first
                           system molecule; ISMO-2; Incyte clone 2849752; diagnosis;
                                                                                                         protein;
                                                                   entry)
                   cell
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                   proliferation;
                                               ISMO-2.
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immune system disorder

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                                                                                       30-JUN-1998;
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/note= "conserved Ig/MHC protein block"
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                                                                                                                                                 'note= "Protein kinase C
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Immune system molecules of disorders associated

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                                                               CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fix mallgnant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
                                                                                                                    antiarthritic; immunosuppressive; antidiabetic; antineuroprotective; hinge region; immunoglobulin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               trauma. It shows homology to vertebrate immunoglobulin gamma heavy-chain. The present sequence is useful in the diagnosis, treatment and prevention of disorders associated with the immune system and cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is an immune system molecule, ISMO-2 from an clone 2849752 isolated from the human breast tumour cDNA library (BRSTTUT13). This sequence is expressed in several libraries, gen those associated with cancer, cell proliferation, immune response
                                                                                                                                                        Binding domain; immunoglobulin; fusion protein; cytostatic;
                                                                                                                                                                                           Binding
 Unidentified
                                  type I diabetes
                                                                                                                                                                                                                             15-JAN-2004
                                                                                                                                                                                                                                                              ADD25783;
                                                                                                                                                                                                                                                                                                ADD25783 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 470
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                                                  rheumatoid arthritis; myasthenia gravis; Grave's disease;
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                                                                                                                                                                                         domain-immunoglobulin fusion protein-associated protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGNQ-----GSFLTKGPSKLNDRADSRRSL---WDQGNFPLIIKNLKIEDSDTYICEVED 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCTVSGGSIRSYYW---NWIRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHLLLVLQLALLP-----AATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI
                                                                                                                                                                                                                                                                                                                                                                                       KSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----KTLSVS------QLELQDSG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPGKGLEWIGYIYTSGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.3%; ilarity 57.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ξ
                                                                                                                                                                                                                           (first entry)
                                  mellitus; multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----NATTTTVWTSGAKGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGC
                                                                                                                                                                                                                                                                                                                                                                                                                        431
                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEGLHNHYTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                  492
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Pred. No. 4.1e-63;
B; Mismatches 98;
                                                                                                                                                                                                                                                                                                B
                                    sclerosis; autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proliferation,
                                                                                                                    antithyroid;
eavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                           #157.
                                                                                     fixation;
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US2003118592-A1

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CC comprising a binding domain polypeptide, that is fused to an Comprising a binding domain polypeptide, an immunoglobulin heavy chain CC comprising a binding domain polypeptide, an immunoglobulin heavy chain CC content region polypeptide that is fused to the hinge region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide, and that is fused to the hinge region polypeptide, a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the first cysteine residues, contains 2 cysteine residues, where the first cysteine residues, and contains 2 cysteine residues, where the first cysteine residues, and contains no more than one (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one (cysteine residues, and a mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one (a) having 3 or more cysteine residues; where complete and a mutated human IgG1 immunoglobulin hinge region polypeptide contains to cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains to cysteine residues; where cysteine residues; where cysteine residues; where cysteine residues; where cysteine residues; where cysteine residues; where cysteine residues; where complete the cell mediated cytocoxicity (ADCC) and complement fixation. The binding domain-immunoglobulin fusion protein is completed and a carrier; and complement fixation construct, producing the binding domain-immunoglobulin fusion protein, a pharmaceutical composition comprising the binding domain-immunoglobulin fusion protein, a malignant condition or a B-cell disorder. The binding domain immunoglobulin fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-2001; 2001US-0367358P
17-JAN-2002; 2002US-00053530
03-JUN-2002; 2002US-0385691P
                                                                                                                                                                                                                                     Sequence
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                                                                             Local Similarity
nes 279; Conserv
μ
                                                                                                                                                                                                                                             492
MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JA.
                                                                                 Conservative
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                                                                                                      47.3%;
55.8%;
                                                                         Score 1279; DB 7;
Pred. No. 4.3e-63;
3; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thompson
                                                                                                                                                       Length 492;
                                                                             Gaps
60
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-TOSPTTIAASPGEKVTITCRASSSVSYMYWYQQKS---

62

The present invention describes an antibody, which can react specificall with ganglioside GD2, and is transplanted with a human type complementation-determining domain (CDR), or its fragments. The antibody

react specifically

Page 111-114; 123pp; Japanese

Human type complementation-determining domain transplanted antibody and derivatives against ganglioside GD2, useful in diagnosis and therapy of e.g. tumors, has low antigenicity, little side effects but potent activity in cancer.

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RESULT 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUL-2001
                                                                                                                                                                                                                                                                                                                                                               Hanai N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ganglioside GD2 specific antibody related protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB81972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse; cancer.
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                                                                                                                                                                                                                                                                                                           2001-266163/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
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                                                                                                                                                                                                                                                                                                                                                            Shitara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                  Nakamura
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Best Local (
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17-JAN-2001;
17-JAN-2002;
03-JUN-2002;
                                                                                                                                                                                Binding domain; immunoglobulin; fusion protein; cytostatic; antitarthritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and its derivatives are useful in diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used the exemplification of the invention
                                                           25-JUL-2002;
                                                                                                                         US2003118592-A1
                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                           Binding domain-immunoglobulin fusion protein-associated protein
                                                                                                                                                                                                                                                                                                                                                           15-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG------LQLDETCAEAQ 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVKPSQTLSITCTVSGFSLASYNIHWVRQPPGKGLEWLGVIWAGGSTNYNSALMSRLTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGKKGDTVELTCTAS -- OKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL-
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2001US-0367358P
2002US-00053530
2002US-0385691P
                                                           2002US-00207655
                                                                                                                                                                                                                                                                                                                                                         (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                       protein; 543
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Pred. No. 5.5e-63;
25; Mismatches 96;
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61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQG-NFPLIIKNLKIEDSDTYICE------

-GASPKLWIYDTSKLASGVPNRFSGSGSGTSYSLAINTMETEDAATYYCQQWSSTPLTF

120 151

110 62

- SEVOLLVFGLTANSDTHLLQGQSLTLTLESPPGSSP

1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

TQSPTTIAASPGEKVTITCRASSSVSYMYWYQQKS---

Matches Query Match Best Local (

279;

Conservative

Similarity

47.3%; 55.8%;

; Score 1277; DB 7; ; Pred. No. 6.2e-63; 33; Mismatches 92;

92;

96;

Gaps

Length Indels

domain

19

MSRGVD---

Sequence 543

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152

SVQ-CRSPRGKNIQ----

GGKT--

-LSVSQLELQDSGT

GSGTKLEIKRGGGGSGGGGGGGGGQVQLKEAGPGLVQPTQTL---SLTCTVSGFSLTSD

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The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide, an immunoglobulin hange region polypeptide, an immunoglobulin heavy chain CC polypeptide, and an immunoglobulin heavy chain CT constant region polypeptide that is fused to the hinge region CC polypeptide, and an immunoglobulin heavy chain CT constant region polypeptide comprises: a wild-type human IgG1 Immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the first cysteine is not mutated; a contains 2 cysteine residues, where the first cysteine is not mutated; a cutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (b) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (c) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (c) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (c) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (c) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide contains on cysteine residues. The binding domain-immunoglobulin hinge region polypeptide or an isolated polymucleotide encoding the construct comprising the polymucleotide (perably linked to a promoter), c a host cell transformed or transfected with a recombinant expression construct producing the binding domain-immunoglobulin fusion protein, a promoter, and treating a subject to having or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein or a binding domain and constinued domain condition or a binding domain con
sclerosis or autoimmune disease. The present sequence is a binding doma -immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at sequence and electronic format directly from the sequence in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 345; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayden-Ledbetter MS,
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RESULT 53
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The invention relates to an anti-Abeta (amyloid-beta peptide) antibody 266. The antibodies are useful for treating and preventing conditions associated with the Abeta peptide, such as Alzheimer's disease, Down syndrome, and cerebral amyloid angiopathy; for disgnosing diseases in humans; for determining whether a human subject will respond to treatment using humanized antibodies against Abeta; for treating, preventing and reversing cognitive decline in clinical or pre-clinical Alzheimer's disease, Down's syndrome or cerebral amyloid angiopathy; for inhibiting formation of amyloid plaques of the effects of toxic soluble Abeta species in humans. Treatment of the patients with antibody will inhibit or prevent cognitive decline typically associated with disease
                                                                                                                                                                                                                                                New antibodies comprising a heavy chain and a light chain complementarity determining regions from antibody 266, for treating and preventing conditions associated with the A beta peptide, e.g. Alzheimer's disease
                                                                                                                                                                                                    Disclosure; Fig 6; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-2001; 2001US-0313224P
                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2002; 2002WO-US021322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                           Tsurushita N,
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RESULT 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-Abeta antibody 266 N56S heavy chain
WPI; 2003-278557/27
                    Jia AY,
                                                                                                                                                                                                           Hu266 N56S
                                                                17-AUG-2001; 2001US-0313224P.
                                                                                      14-AUG-2002; 2002WO-US021322.
                                                                                                            27-FEB-2003
                                                                                                                               WO2003016466-A2
                                                                                                                                                     Homo sapiens
                                                                                                                                                                                      Amyloid-beta;
                                                                                                                                                                                                                                 18-AUG-2003
                                                                                                                                                                                                                                                                          ABR39843 standard;
                                                                                                                                                                         immunostimulant.
                                          (ELIL )
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                                           TILLY & CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         461 AA;
                    Tsurushita N,
                                                                                                                                                                                                                                                                                                                                             NHYTOKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                       PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKFKDTLMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----QLELQDSG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKGLELVAQINSVGSSTYYPDTVKGRFTIS-RDNAKNTLYLOMN-----SLRAEDTAVY
                                                                                                                                                                                                                                                                                                                                 NHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                           PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH
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                                                                                                                                                                                      antibody 266; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----ASGD---YWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGT
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                     Vasquez
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Pred. No. 6.3e
31; Mismatches
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                                                                                                                                                                                     neuroprotective;
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RESULT 5:
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Best Local :
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 02-APR-2003
                                                               AAE33444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibodies comprising a heavy chain and a light determining regions from antibody 266, for treating conditions associated with the A beta peptide, e.g.
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                                                                                                                                                                   NHYTQKSLSLSPG
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                                                                                                                                               NHYTQKSLSLSPG
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 (first entry)
                                                              protein;
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57.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel recombinant anti-EpCAM (human epithelial cell adhesion molecule) antibodies comprising an amino acid sequence defining an immunoglobulin light or heavy chain framework region. Sequences of the present invention are useful for the diagnosis, prognosis and treatment of cancer. They are also used in gene therapy. The present sequence is KS antibody heavy chain-interleukin 2 (IL-2) fusion protein. This sequence is used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant anti-EpCAM antibody having an amino acid sequence defining an immunoglobulin light or heavy chain framework region, for the diagnosis, prognosis and treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 80-82; 82pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer;
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                 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
                                                                           EVHNÄKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                               THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
                                                                                                                                 THTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHBDPEVKFNWYVDGV
                                                                                                                                                                   TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKSCDK
                                                                                                                                                                                              --QLELQDSG--
                                                                                                                                                                                                                        TSVTVSSASTKG--PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
                                                                                                                                                                                                                                                    QSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS----
                                                                                                                                                                                                                                                                                                                                                                 KKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG--SFLTKGPSKLNDRADSRRSLW
 PREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDG
                                                      EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                                                                                                                                                                                               FKGRFAFSLETSTSTAFLQINNLRSEDTATYFC-----VRFISKG-----DYWGQG
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                                                                                                                                                                                                                                                                                                        -LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG
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Pred. No. 8e-63;
9; Mismatches
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SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG---

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                                                                                                           Query Match
Best Local S
Matches 277
                                                                                                                                                                                                                                                                                                                                                  This is the amino acid sequence of a single chain antibody (Sab), termed $$T4$Sab1, comprising an scFv derived from murine monoclonal antibody $$T4$ (see AAW86022) and the human gl constant region. CDNA (see AAV80291) encoding the Sab has been inserted into vector pCIneo to allow expression in mammalian cells. The trophoblast cell surface antigen defined by $$T4$ is expressed at high levels on the cells of a wide variety of human tumours. The invention relates to a vector comprising a nucleotide sequence coding for a tumour interacting protein (TIP) and optionally a nucleotide sequence of interest (NOI) which encodes a protein of interest (POI), the vector being capable of delivering the NOI and/or POI to the tumour recognised by the TIP. Delivery can be in vivo or extenditors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New vector encoding a tumour interacting protein for treating cancer - contains a desired nucleotide sequence and/or protein which recognises tumours, and is used as a gene delivery system to treat cancer.
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kingsman SM,
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20-JUN-1997;
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour interacting protein; cancer; gene therapy; vector; monoclonal antibody; single chain antibody; mouse; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-5T4 single chain antibody
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                                                                                                           Local Similarity
mes 277; Conserv
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                                                     23
                                                                                                                                                                                                                                                                           binding
                                                                                                                                                                                                                                                                        is used to treat cancer, and may also used as a gene delivery for introducing at least 1 gene encoding a TIP (preferably a binding protein) into a haematopoietic cell lineage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV80291
                                                                                                                                                                                                                       595 AA;
                                             TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS
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  TOTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKP----
                                                                                                              Conservative
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97GB-00013150.
97GB-00014230.
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                                                                                                                               47.28;
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Pred. No. 8.8e
18; Mismatches
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                                                                                                         e 1275; DB 2;
. No. 8.8e-63;
ismatches 81;
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------GQSPTLLISYTSS
                                                                                                                                                                 Length 595;
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5T4Sab1.
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                                                                                                           Gaps
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                                      The invention provides human antibodies that bind to stem cell factor (SCF) protein. SCF is also known as mast cell growth factor, steel factor or c-kit ligand. Antibodies of the invention are useful for preparing compositions for treating asthma. They are also used in gene therapy. The present sequence is human SCF antibody heavy chain variable and constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAO31101 standard;
                                                                                                                                                    New purified human antibody that binds useful for preparing a composition for
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   Human; antibody; stem cell factor; mast cell growth factor; asthma; steel factor; c-kit ligand; gene therapy.
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                                                                                                                            Claim 9;
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                                                                                                                         Page 47; 94pp;
                                                                                                                                                                                                                       T, Tomkinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
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Sequence

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RESULT 58
ABR39844
ID ABR39844
ID ABR39844
AC ABR39
XX ABR39
XX AMP166
XX AMP16
XX AMP16
XX HOMO
XX HOMO
XX HOMO
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XX ARP1;
DR WPI;
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                                                                        New antibodies comprising a heavy chain and a light chain complementarity determining regions from antibody 266, for treating and preventing conditions associated with the A beta peptide, e.g. Alzheimer's disease
                                                                                                                                                                                WPI; 2003-278557/27
N-PSDB; ACC47228.
                                                                                                                                                                                                                                                                                                                                                            17-AUG-2001; 2001US-0313224P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amyloid-beta; Abeta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hu266 N56T heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR39844 standard;
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                                                     Down
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL 383
                                                                                                                                                                                                                                                           Tsurushita N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCOKTHICPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCDXTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----QLELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPK 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                              ELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody 266; nootropic; neuroprotective; CDR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.2%; Score 1274.5; DB
59.2%; Pred. No. 6.9e-63;
tive 27; Mismatches 67
                                                                                                                                                                                                                                                           Vasquez
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Disclosure; Fig 3; 82pp; English

RESULT 59
ABR39848
ID ABR39
XX
AC ABR39
XX
DT 18-AU
XX
Hu266
XX
Amylc
XW Amylc
XX
OS Homo
XX

18-AUG-2003 ABR39848;

(first entry)

ABR39848 standard; protein;

461

₿

Hu266 N56T heavy chain

Amyloid-beta; Abeta; antibody 266; nootropic; neuroprotective; CDR;

Homo sapiens

mmunostimulant

5 밁 S

448 419 388 359

NHYTQKSLSLSPG

431 460

PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH

418

PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH

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Best Local Similarity
Matches 281; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an anti-Abeta (amyloid-beta peptide) antibody 266. The antibodies are useful for treating and preventing conditions associated with the Abeta peptide, such as Alzheimer's disease, Down syndrome, and cerebral amyloid angiopathy; for diagnosing diseases in humans; for determining whether a human subject will respond to treatment using humanized antibodies against Abeta; for treating, preventing and reversing cognitive decline in clinical or pre-clinical Alzheimer's disease, Down's syndrome or cerebral amyloid angiopathy; for inhibiting formation of amyloid plaques of the effects of toxic soluble Abeta species in humans. Treatment of the patients with antibody will inhibit or prevent cognitive decline typically associated with disease progression and reverses it. The present sequence represents a humanised anti-Abeta antibody 266 N56T heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 461 AA;
 328
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                                                                            268
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LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY
                       LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFY
                                                                                              SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
                                                                                                                                                                                    CTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMI
                                                                                                                                                                                                                                                                                                                                          ICEVEDOKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNS--
                                                                          SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW
                                                                                                                                                     CNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI
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                                                                                                                                                                                                                                                                     -----KTLSVS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antibodies comprising a heavy chain and a light chain complementarity determining regions from antibody 266, for treating and preventing conditions associated with the A beta peptide, e.g. Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                CNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI
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                  PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the coding and protein sequences for a number of human immune system associated proteins (HISAPS). These can used in the diagnosis and treatment of various autoimmune disorders, infections and cell proliferation diseases. The diseases include AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human immune system associated proteins (HISAP) encoding the HISAP, useful for diagnosing, treating or cell proliferative disorders or infections.
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N-PSDB; AAC66522.
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Hillman JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 473
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The present invention relates to domain deleted CC49 or C2B8 antibodies. Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain deleted sequence in which CH2 domain has been deleted and are reactive with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive with CD20 and comprise a heavy chain having a sequence of a derived domain deleted C2B8 construct where the CH2 domain has been deleted. Sequences of the invention are useful for imaging a neoplasm. They are also useful for treating myelosuppressed patients suffering from Hodgkin's lymphoma. Antibodies of the invention are also used to treat neoplastic disorder such as haematologic neoplasm, preferably non-lodgkin's lymphoma. Antibodies of the invention are also used to treat neoplastic disorder, colon cancer and haematologic malignancy. They are useful for reducing tumour size, inhibiting tumour growth and/or prolonging the survival time of tumour-bearing animals and for treating
                                                                                                                                                                                                                                                           Novel domain deleted CC49 antibody reactive with tumor associated -72, or C2B8 antibody reactive with CD20, useful for treating myelosuppressed patient suffering from a neoplastic disorder.
                                                                                                                                                                                                                                                                                                                                                                                Braslawsky GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2001;
16-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         non-Hodgkin's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neoplasm;
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                                                                                                                                                                                                                                    Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC49 antibody; C2B8 antibody; tumour associated antigen; sm; neoplastic disorder; haematologic neoplasm; colon canodgkin's lymphoma; haematologic malignancy; tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibody
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2001US-0331481P
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                                                                                                                                               SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES
                                                                                                                                                                                                           VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
                                                                                                                                                                                                                                                          NTKVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                                                                                                                                                                                                                                                                            EFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLLVLQLALLPAATQGNKVVLGKKG-----DTVELTCTASQKKSIQF--HWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is human C5E10 heavy chain protein. is used in the exemplification of the invention
                              SPG 431
                                                                            NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
                                                                                                                                                                                           VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
                                                                                                                                                                                                                                                                                                                      FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPS
                                                                                                                                                                                                                                                                                                                                                      --KTLSVS-----TWTCTVLQNQKKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILGNQGSFLTKGPSKLNDRADSRRSL-WDQGNFPLIIK--NLKIEDSDTYICEVEDQKEE 117
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                                                             NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
                                                                                                                           SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES
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                                                                                                                                                                                                                                                                                                                                                                                       -ARCYYGSSPYFD---YWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.2%;
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Pred. No. 7
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7.8e-63;
hes 95;
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CSE10; antibody; cytostatic; antiallergic; antianemic; antiasthmatic; vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic; thyromimetic; hepatotropic; haemostatic; antileprotic; antibacterial; neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulo
                                      29-JAN-2002;
                                                                                                                                                                                                      31-MAR-2003
                                                                                                                                                                                                                                             ABB82837 standard;
                                                                               WO200296948-A2
                                       2002WO-US002374
                                                                                                                                                                                                                                             protein;
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29-JAN-2001; 16-NOV-2001; 21-DEC-2001;

2001US-0264318P 2001US-0331481P 2001US-0341858P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC The invention relates to a dimeric antibody (I) comprising several CC monomeric subunits, where the monomeric subunits are non-covalently CC associated. (I) is useful for treating a disorder, especially immune CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease, CC resistant Hodgkin's disease high grade, low grade and intermediate grade CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL), CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma, CC lymphoma (FL), diffuse large cell lymphoma, angioimmunoblastic CC lymphoadenopathy, small lymphocytic B cell lymphoma, angioimmunoblastic CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma, CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small CC cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a CC detailed description of the various uses of (I)). The present sequence CC represents the antibody CSE10 heavy chain
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 468 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Fig 6; 78pp;
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                                   SPG 431
                                                                       NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
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                                                                                                                                                                                                                      VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
                                                                                                                                                                                                                                                                                                                                                                                                      --KTLSVS---
                                                                                                                                                                                                                                                                                                                                                                                                                                        -ARCYYGSSPYFD---YWGQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 170
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                                                                                                                                                                                                                                                                                                                                                                                                    ----QLELQDSG------TWTCTVLQNQKKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1274; DB 6;
Pred. No. 7.8e-63;
8; Mismatches 95;
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Best Local Similarity
Matches 275; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a compound comprising CD44 specific antibody molecule conjugated to a highly cytotoxic drug, which cleaves under intracellular conditions. The compound is used in pharmaceutical composition for the treatment of cancer, solid tumours, and as an adjuvant to surgical intervention to treat minimal residual disease. The present sequence is humanised murine antibody BIWA4 heavy chain protein used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New compound useful for treatment of cancer comprises CD44 specific antibody molecule conjugated to a highly cytotoxic drug, which cleavunder intracellular conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD44; cytotoxic drug; therapy; cancer; tumour; minimal residual disease; antigen; cytostatic; BIWA4 antibody; murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised murine antibody BIWA4 heavy chain protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE35327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 15-16; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1258255-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAD53977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adolf G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAY-2001; 2001EP-00112227
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              EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                                                                                                                                                S-RDNAKNSLYLOMN-----SLRAEDTAVYYCARQ-----GLD-----YWG
                                                                                                                                                                                                                                                                                                                  LGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKILGNQGSFL----TKGPSKL
                                                                    THTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGV
                                                                                                              TFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK
                                                                                                                                          --QLELQDSG---
                                                                                                                                                                       RGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
                                                                                                                                                                                                   QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS-----
                                                                                                                                                                                                                                                         NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG
                                                                                                                                                                                                                                                                                     LVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYYLDSIKGRFTI
EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
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                                                                                                                                                                                                                                                                                                                                             47.1%; Score 1273.5; ilarity 59.3%; Pred. No. 7.8e Conservative 27; Mismatches
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                                                                                                                                         ----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK
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                                                                                                                                                                                                                                                                                                                                                             5; DB 6;
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RESULT 64
AAB34876
ID AAB34
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                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to novel antibody molecules comprising a variable region of the heavy (VH) and/or light chain (VL) of CD44v6 specific humanised antibody called BIWA8 and BIWA4. Sequences of the invention are useful for manufacturing a medicament and for treating cancer including colorectum, non-small cell lung, breast, head and neck, ovarian, lung, bladder, pancreatic cancer or metastatic cancers of the brain. They are also useful in antibody therapy. The present sequence is BIWA4/8 antibody heavy chain mature protein. This sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibodies specific for an epitope coded by the variant exon of the CD44 gene, useful for treating cancer, including non-small cell lung, breast, head and neck, ovarian and lung cancer.
                                                                                                                                                                                                                                                                                                                                                                  Sequence 444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 24; Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-129413/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miglietta
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26-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAY-2002; 2002WO-EP005467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIWA8 antibody; heavy chain variable region; light chain variable region; VH; VL; CD44v6; medicament; cancer; antibody therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIWA4/8 antibody
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BOEHRINGER INGELHEIM PHARM INC
QSLTLTLESPPGSSPSVQCRSPRGKNIQGG----
                                                S-RDNAKNSLYLOMN-----SLRAEDTAVYYCARQ-----
                                                                                                                                                                                                     LGKKGDTVELTCTAS--OKKSIQFHW-----KNSNQIKILGNQGSFL----TKGPSKL
                                                                                                    NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG
                                                                                                                                                    LVKPGGSLRLSCAASGFTFSSYDMSWVRQAPGKGLEWVSTISSGGSYTYYLDSIKGRFTI
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JJ, Van D
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                                                                                                                                                                                                                                                              Conservative
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2001US-0325147P.
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Van Dongen AAMS;
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                                                                                                                                                                                                                                                                                 47.18;
59.38;
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                                                                                                                                                                                                                                                        Score 1273.5; DB 6;
Pred. No. 7.8e-63;
7; Mismatches 69;
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----KTLSVS---
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                            Length
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                                                ·GLD-----YWG
                                                                                                                                                                                                                                                                                                              444;
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                                                                                                                                                                                                                                                           Gaps
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RESULT 65
AAR93553
ID AAR93
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                                                                           The sequences given in AAR93553-54 represent the heavy and light chains respectively of a monoclonal antibody against a 65 kD antigen of human cytomegalovirus (hCMV). The DNA's encoding these sequences were amplified using the sequences given in AAT18040-58. The monoclonal antibody may be used in the diagnosis of hCMV
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N-PSDB; AAT18059.
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                                                                                                                                                                                                                                                                                                                        Claim 4; Page 16-18; 22pp; Japanese
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NISSHINBO
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Best Local Similarity
Matches 283; Conserv
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                                                                                           note= "complementarity determining
                                                                                                          'label= CDR1
                                                                                                                                                                        label= Leader_peptide
                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
                                                                                                                                                                                                                                                                                                                                                                                       475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1273.5; DB 2;
Pred. No. 8.4e-63;
9; Mismatches 98;
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                                                    region
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             region
                                                                                           region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77;
               ٥
                                                                                                                                                                                                                                                                                 virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                 RSV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
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                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 276; Conser
                                                                                                                                                                                                                                                                                                                                                                                                             A polypeptide (AAW11641) comprises a leader sequence, RF-2 heavy chain variable region (see also AAW11635), and human gamma 1 constant region. RF-2 is a human monoclonal antibody (hMAb) specific for the fusion protein of respiratory syncytial virus (RSV). The polypeptide can be produced in eukaryotic host (e.g. CHO) cells transfected with vector NEOSPLA incorporating a DNA construct (AAT61279) including the RF-2 VH sequence. RF-1 and RF-2 heavy and light chains (see also AAW11638-40) are similarly produced. The transfected host cells provide a constant, stable supply of anti-RSV F-protein hMAbs for use in the treatment or prevention of RSV infection
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 6; Fig 11b-c; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human monoclonal antibody specific for respiratory protein - used for the prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT61279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brams P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
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                                                                                                                                                                         125
                292
                                                                                                                                               167
                                                                                                                                                                                                   118
                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                              70
                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                        10 LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS----QKKSIQFHWKNSNQIKIL---
                            VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
                                                                                 EFKIDIVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                                                                                                                                                                                                                              ARIDWDDDTFYSASLKTRLSISKDTSKN-----QVVLRMTNVDPVDTATYFCARASLYDS
                                                                                                                                                                                                                                                                              LVAVATRVLSQVQLQESGPALVKPTQTLTLTCTFSGFSLSTRGMSVNWIRQPPGKALEWL
                                                                NTKVD----KKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV
                                                                                                                  FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPS
                                                                                                                                                                         DSFYLF-----YHAYWGQGTVVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
                                                                                                                                                                                                   VQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------
                                                                                                                                                                                                                                                    ----GNOGSFLTKG-PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEE
             UDVSHEDPEVKFNWYVDGVEVHNAKTKPRBEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV
                                                                                                                                               --KTLSVS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chamat SS,
                                                                                                                                                                                                                                                                                                                                  47.1%; Score 1273.5; ilarity 57.1%; Pred. No. 8.46 Conservative 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-00488376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-US010070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= K~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119. .134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "complementarity determining region
135. .145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= FR3
/note= "framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "human gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "framework"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= FR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŗ,
                                                                                                                                              ---OLELODSG-------TWTCTVLQNQKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Walsh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               constant region"
                                                                                                                                                                                                                                                                                                                                                5; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heard
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                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      syncytial virus fusion RSV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Newman
                                                                                                                                                                                                                                                                                                                                                              475;
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79;

Gaps

11;

69

248

291

308

351

193 177 166 124

235

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RESULT 67
AAY97172
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Novel fusion protein constructs comprise a fibroblast growth factor (FGF) receptor (FGF-R) extracellular domain (ECD) lacking the immunoglobulin (Ig) I segment fused to a heterologous oligomerization domain that comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4 region, or light chain of an immunoglobulin molecule, or a peptide with a leucine zipper motif. The Ig I segment is not necessary for binding of
                                                                                                    New polypeptide comprising a fibroblast growth factor receptor extracellular domain fused to a heterologous oligomerization doma treating FGF-, angiogenesis-, or FGF receptor-mediated disorders.
                                                                                Claim 14; Page 58-59; 70pp; English.
                                                                                                                                                      N-PSDB; AAA52129
                                                                                                                                                                                     Kavanaugh WM,
                                                                                                                                                                                                                                    08-FEB-1999;
                                                                                                                                                                                                                                                         07-FEB-2000; 2000WO-US003166
                                                                                                                                                                                                                                                                                 10-AUG-2000
                                                                                                                                                                                                                                                                                                       WO200046380-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ophthalmological; anti-proliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1; immunoglobulin; G1; oligomerization domain; Fc region; fusion protein inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY97172 standard; protein;
                                                                                                                                                                                                             (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                2000-514961/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Extracellular domain-Ig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                      Ballinger
                                                                                                                                                                                                                                    99US-0119002P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                /label= FGF-R1_extracellular_domain
/note= "The Ig I segment and acid be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= FGF-R1_signal_peptide
                                                                                                                                                                                                                                                                                                                                                                label=
                                                                                                                                                                                                                                                                                                                                                                                  'label= Ig_III_segment
                                                                                                                                                                                                                                                                                                                                          label=
                                                                                                                                                                                                                                                                                                                                                                                                             label=
                                                                                                                                                                                                                                                                                                                                                    .497
                                                                                                                                                                                                                                                                                                                                                                           . 265
                                                                                                                                                                                                                                                                                                                           - Human IgG1 Fc region
"Contains hinge region and
                                                                                                                                                                                                                                                                                                                                                                Linker
                                                                                                                                                                                                                                                                                                                                                                                                          Ig_II_segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fc fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                    χοσ
                                                                                                                                                                                                                                                                                                                              domains CH2 and
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                                                                                                                   domain
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Best Local S
Matches 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the affinity for aFGF and heparin, protects the core of the molecule from proteolysis, and abrogates the heparin requirement for aFGF binding. The new fusion polypeptides are better FGF inhibitors than FGF-R monomer proteins. The FGFR-Ig Fc fusion dimers are active as FGF antagonists at subnanomolar concentrations and were 20-fold more potent than the FGF-R monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The fusion constructs are useful to treat FGF-, angiogenesis-, or FGF-R. The fusion constructs are useful to treat FGF-, angiogenesis-, or FGF-R mediated disorders, such as tumourigenesis (e.g. bladder, breast, lung, rectal, testis and cervical tumours), neovascularization (e.g. diabetic retinopathy, neovascular glaucoma, wound healing and corneal scarring) and byper-proliferation of vascular smooth muscle cells (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      postangioplasty and postatherectomy restenosis)
       437
                                             372
                                                                                  377
                                                                                                                                                                                                252
                                                                                                                                                                                                                                                                                                                                                      164
                                                                                                                                                                                                                                                                                                                                                                                           140
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                           PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                 SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLHAVPAA-----KTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW-KNSNQIK----ILGNQGSFL 69
                                                                                                      ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
                                                                                                                                                                                                                                                                                                                                                    -- QGGKTLSVSQLELQDSGTWTC------
                                                                                                                                                                                                                                                                                                                                                                                                                             FGLTANSDTHLLQGQSLTLTLESPP-----GSS-----PSVQCRSPRGKNI 163
PENNYKTTPPVLDSDGSFFLXSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                           SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
                                                                                                                                                                                                                                      EGSGSPGLQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                           -----APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                                                TDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLE---ALEERPAVMTSPLYL
                                                                                                                                                                                                                                                                                                                                                                                       AGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TWSIIMDSVVPS----
                                                                                    ALPAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKG-----P$KLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA,
                                                                                EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.1%;
57.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----DKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQ 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1273.5;
Pred. No. 8.8e
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.5; DB 3;
. 8.8e-63;
cches 83;
                                                                                                                                                                                                                                                                                                                                                  -----TVLQNQKKVEFKIDIVPCP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                311
                                           431
                                                                                                                                                                                                                                      316
                                                                                                                                                                                                                                                                           251
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                                                                                                                      371
                                                                                                                                                           376
                                                                                                                                                                                                                                                                                                              256
                                                                                436
                                                                                                                                                                                                                                                                                                                                                      203
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RESULT 68
AAY97171
     Homo
                                                                        immunoglobulin; G1; oligomerization domain; Fc region; foinhibitor; dimer; antagonist; cytostatic; anti-diabetic; ophthalmological; anti-proliferative.
                          Key
                                                                                                                                                            04-DEC-2000
                                                                                                                                                                                                            AAY97171 standard;
                                                                                               FGF-R; fibroblast growth factor receptor; extracellular domain; IgG1; immunoglobulin; G1; oligomerization domain; Fc region; fusion protein
                                                                                                                                                                                    AAY97171;
                                                  sapiens
                                                                                                                                     FGF-RI
                                                                                                                                     Extracellular
                                                                                                                                                            (first entry)
Location/Qualifiers
1. .21
/label= FGF-R1_signal_peptide
                                                                                                                                                                                                            protein;
                                                                                                                                    domain-Ig Fc fusion protein
                                                                                                                                                                                                            525
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protein;

Peptide

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                                                                                                                                                                                                                                                                                                                                                                                                   CC receptor (FGF-R) extracellular domain (EGD) lacking the immunoglobulin (CI) I segment fused to a heterologous oligomerization domain that (CI) I segment fused to a heterologous oligomerization domain that (CC comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4 (CC comprises an immunoglobulin Fc region, hinge region, CH1, CH2, CH3 or CH4 (CC region, or light chain of an immunoglobulin molecule, or a peptide with a CC leucine zipper motif. The Ig I segment is not necessary for binding of CC acidic FGF and basic FGF (bFGF). The Ig I deletion further increases the affinity for aFGF and heparin, protects the core of the molecule from CC proteolysis, and abrogates the heparin requirement for aFGF binding. The CC mew fusion polypeptides are better FGF inhibitors than FGF-R monomer roteins. The FGFR-Ig Fc fusion dimers are active as FGF antagonists at subnanomolar concentrations and were 20-fold more potent than the FGF-R CC monomer protein as competitors of bFGF binding to immobilized FGF-Rs. The fusion constructs are useful to treat FGF-, angiogenesis-, or FGF-R-CC mediated disorders, such as tumourigenesis (e.g. bladder, breast, lung, crectal, testis and cervical tumourigenesis (e.g. bladder, breast, lung, crectal, testis and cervical tumourigenesis (e.g. bladder, breast, lung, crectal, testis and cervical tumourigenesis (e.g. bladder, breast, lung, crectal, testis and cervical tumourigenesis (e.g. bladder, breast, lung, crectal, testis and carrior) and more above the machine astronesis (e.g. diabetic rectal or testis and carrior) and more above the machine astronesis (e.g. diabetic rectal or testis and carrior) astronesis (e.g. diabetic rectal or testis and carrior) astronesis (e.g. diabetic rectal or testis and carrior) astronesis (e.g. diabetic rectal or testis and carrior) and more above the machine astronesis (e.g. diabetic rectal or testis and carrior) astronesis (e.g. diabetic rectal or testis described experisor) and corneal scarring) and corneal scarring)
                                                                                                                                                                                                                                                          Matches 276;
                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                               Sequence 525 AA;
                                                                                                                                                                                                                                                                                                                                                                                      postangioplasty and postatherectomy restenosis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 14; Page 54-55; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAA52128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kavanaugh WM,
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  168
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                                                                                                                                                                       73
                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                QLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW-KNSNQIK----ILGNQGSFL
                                          FGLTANSDTHLLQGQSLTLTLESPP------
                                                                                                                                                                     KLHAVPAA-----KTVKFKCPSSGTPNPTLRWLKNGKEFKPDHRIGGYKVRYA
AĞLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNĞSKIGPDNLPYVQILKTAĞVNT
                                                                                                                           TKG-----PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV 122
                                                                                                                                                                                                                                                             Conservative
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/label= FGF-R1_extracellular_domain
/note= "Ig I segment is deleted"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Human_IgG1_Fc_region
/note= "Contains hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= Ig_III_segment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig_II_segment
                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                               Score 1273.5; DB 3; Pred. No. 9.4e-63;
                                                                                                                                                                                                                                                             Mismatches
                                                                                  -DKGNYTCIVENEYGSINHTYQLDVVERSPHRPILQ
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                                                                                                                                                                                                                                                             83;
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                                      -GSS-----PSVQCRSPRGKNI 163
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                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                       525;
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                                                                                                                                                                                                                                                             Gaps
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WPI; 2000-514961/46

Kavanaugh WM,

Ballinger CORP.

(CHIR) CHIRON

07-FEB-2000; 2000WO-US003166

99US-0119002P

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RESULT 69
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FGF-R; fibroblast growth factor receptor; extracellular domain; IgG
immunoglobulin; G1; oligomerization domain; Fc region; fusion prote
inhibitor; dimer; antagonist; cytostatic; anti-diabetic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY97170 standard;
                                                                                                                                                                                                                                                          Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ophthalmological; anti-proliferative.
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                                                                                                                                                                                      Protein
                                                                                                                                                                                                                       Peptide
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                                                                                                                 10-AUG-2000
                                                                                                                                        WO200046380-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 --QGGKTLSVSQLELQDSGTWTC------TVLQNQKKVEFKIDIVPCP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGPYPSDIAVEWESNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLE---ALEERPAVMTSPLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGSGSPGLQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry
                                                                                                                                                                                                                                                                                  126. . . /
/label=
/2
                                                                                                                                                                                                                                  /label= Ig_III_segment
/note= "This is the IIIc variant version"
                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                               /label= Human IgG1 Fc_region
/note= "Contains hinge region
                                                                                                                                                                                                                                                                                                                                       label= FGF-R1_extracellular_domain
                                                                                                                                                                                                                                                                                                                                                              label= FGF-R1_signal_peptide
                                                                                                                                                                                                note= "Contains trhombin cleavage
                                                                                                                                                                                                                                                                     label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                          . 339
                                                                                                                                                                                                                                                                                 . 228
                                                                                                                                                                                                                                                                                                                               101
                                                                                                                                                                                      . 622
                                                                                                                                                                                                                                                                Ig_II_segment
                                                                                                                                                                                                                                                                                                                 Ig_I_segment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptide comprising a fibroblast growth factor receptor extracellular domain fused to a heterologous oligomerization domatreating FGF-, angiogenesis-, or FGF receptor-mediated disorders.
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                                                                                                                                                                                                                                                                                            378
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 618
                                   428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
LSPG
                                   Past
                                                                    SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
                                                                                                                                                             VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 367
                                                                                                                                                                                                                                       VVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDMLNGKEYKCK 307
                                                                                                                                                                                                                                                                                            GLVPRGSGSPGLQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
                                                                                                                                                                                                                                                                                                                DIVP----CPA-PEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCV
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                                                                                                                                                                                                                                                                                                                                                                DKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVLEALEERPAVMTSPLYLESRG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                        GLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNTT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKLNDRADSRRSLW-----
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                                                                                                                                                                                                                  VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK
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   621
                                   431
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57.0%;
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k; Pred. No. 1.1e
31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
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RESULT 70 AAB83838

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RYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQD

YNSPPTFG

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                                                                                                  Query Match
Best Local
                                                                                                                                                              The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders including Parkinson's disease, periodontal diseases, cardiopulmonary diseases, cardiovascular diseases, pastrointestinal disorders, infections, diabetes, Helicobacter-related diseases, and other immune disorders. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-NOV-1999;
15-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                       Use of single chain antibody capable of recognizing a disease molecule for manufacturing a medicament for preventing and/or disease condition associated with disease associated molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single chain antibody; ScFv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; harkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes
                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-343805/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kingsman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200136486-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter-related disease; immune disorder.
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                                                                                                  Similarity
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     R-RSLWDQ-----GNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL
                                                        TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS
                                                                                      Conservative
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2000GB-00005071.
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                                                                                                47.1%;
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9; Mismatches 81;
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treating a
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This invention relates to a new antibody library which comprises at let 100 cells, each of which comprises at least one integrated retroviral vector expressing an antibody light or heavy chain. Antibodies are of increasing importance in human therapy, assay procedures and diagnosti methods and a need exists for efficient methods of generating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAR-2002; 2002US-0368808P
10-APR-2002; 2002US-0371299P
28-MAR-2003; 2003US-00371299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody library; retroviral vector;
antibody heavy chain; human therapy;
plasmid; GATEWAY vector; LL2HCF.
                                                                                                                                                                                                                           New antibody library comprising cells comprising at least one integrated retroviral vector expressing an antibody light or heavy chain, useful in
                                                                                                                                                                                                                                                                                                           WPI; 2003-804051/75.
N-PSDB; ADE64205.
                                                                                                                                                     Disclosure;
                                                                                                                                                                                                    preparing a
                                                                                                                                                                                                                                                                                                                                                                                     Breme1
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                                                                                                                                                                                                    for diagnosing
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multiplicity of infection;
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Best Local Similarity
Matches 270; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              screening antibody libraries containing large numbers of antibodies. The antibody library of the invention addresses this need, with the additional advantage of strict control over multiplicity of infection (MOI), and is useful in preparing a composition for diagnosing or treating a wide variety of disorders. The present sequence is the amino acid sequence of the LIARICF protein, which was encoded by the Gateway retroviral vectors used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                              365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   465
                                                                                                                                                                                                                                                                                                                        VTVSSASTKGPSVFPLAPSSKSXSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
                                                                                                                                                                                                                                                                                                                                                      LTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----QL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQ
                                                                                                                                                                                           PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                                                                                                      VLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKSCDKTHTC
                                                                                                                                                                                                                                                                                      ELQDSG-----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC
                                                                                                                                                                                                                                                                                                                                                                                      ATITADESTNTAYMELSSLRSEDTAFYFCARRD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPGSSVKVSCKASGYTFTSYWLHW-----VRQAPGQGLEWIGYINPRNDYTEYNQNFKDK
YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                  YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                            QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
                                                                              QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
                                                                                                                            AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
                                                                                                                                                        AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP
                                                                                                                                                                                                            ----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.1%; ilarity 58.7%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1272.5;
pred. No. 9.3e
27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; DB 7;
).3e-63;
les 76;
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                              431
464
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                                                                                             391
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AAB49243 standard; protein; 476

Chimeric 4H6 anti-DR4 antibody heavy chain protein. 15-MAR-2001

(first

autoimmune Anti-Death receptor 4 DR4; antibody; apoptosis; cancer; arthritis;

Homo sapiens. Synthetic.

07-DEC-2000

WO200073349-A1

25-MAY-2000; 2000WO-US014599

28-MAY-1999; 99US-00322875

(GETH) GENENTECH INC

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Best Local 9
                humanisation; complementarity determining region; CDR; CDR grafting; reactive stroma; fibroblast; epithelial cancer; diagnosis; immune response; framework sequence; constant region; variable region; producibility; treatment; cancer; colorectal; lung; breast; head; neck; ovarian; lung; bladder; panoreatic; merastasis; detection; wound healing; ovarian; lung; bladder; panoreatic; merastasis; detection; wound healing;
                                                                                                                                                                                                                                                                      17-OCT-2003
31-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to an anti-Death receptor 4 (DR4) antil The antibodies of the invention are useful for inducing apoptosis in mammalian cancer cells such as colon cancer cells and for treating autimmune-related disease in a mammal such as arthritis and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel anti-death receptor 4 antibodies useful for treating cancer immune related disorders such as rheumatoid arthritis, sjogren's syndrome, Grave's disease and diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                             AAY50151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 TVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL-WDQGNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 47.1%;
Similarity 60.4%;
                                                                                                                                                                                                                   F19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPEL
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: | :|: | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        476
                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-----PEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSPSVQCRSPRGKNIQGG------KTLSVS-----QLELQDSG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVFLKMNSLQTDDTAMYYCAREGEFD-----YYGSSLLS-YHSMNFWGQGTSVTVSSAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLSITCTVSGFSLTSYGVHWVRQPPGKGLEWLGVIWAVGSTNYNSALMSRLSISKDNSKS
                                                                                                                                                        monoclonal; F19; fibrinogen activation protein
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                                                                                                                                                                                                                                                                      entry)
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Pred. No. 1e-6:
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P
immunogenicity;
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                                                                                                                                                                                                                (chF19HC)
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                                                                                                                                                                                                                                                                                                                                                                                              CC mouse/human F19 antibody (christic). F19 (ATCC Accession number HB 8269)
CC is a murine monoclonal antibody against fibroblast activation protein
CC alpha (FAP). FAP is a cell surface molecule of reactive stromal
CC fibroblasts, and its induction is a highly consistent molecular trait of
CC the reactive stroma of many types of epithelial cancer. Although F19 may
CC be useful in vitro, e.g., for diagnosis, its applications for in vivo use
CC in humans are problematic as it elicits a human anti-mouse response which
CC reduces the efficacy of the antibody in patients and impairs continued
CC administration. This chimeric antibody was humanised by joining entire
CC murine variable regions to human constant regions. However, humanised
CC antibodies produced by this method can still elicit an anti-mouse
CC response in humans, whereas antibodies humanised via CDR (complementarity
CC determining region) grafting are less immunogenic in humans. Humanised
CC response in humans antibodies are useful for treating cancers e.g., colorectal cancers,
CC ovarian cancers, lung cancers, breast cancers, head and neck cancers,
CC ovarian cancers. They are also useful for the detection of activated
CC stromal fibroblasts in a healing wound, inflamed skin or a tumour in a
CC human patient. (Updated on 17-0CT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                               Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                             W----DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ---GQSLTL 141
                                                                LQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCP
                                                                                                                                                                                                                                                                                               LGKKGDTVBLTCTASQKKSIQF--HWKNSNQIKILGNQGSF-LTKGPSKLNDRADSRRSL
   PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
                                                                                                   LQDSG----
                                                                                                                                  TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 179
                                                                                                                                                                TLESPPGSSPSVQCRSPRGKNIQGG----
                                                                                                                                                                                                                                                                 LVKPGASVKMSCKTSRYTFTEYTIHWVRQSHGKSLEWIGGINPNNGIPNYNQKFKGRATL
                                                                                                                                                                                                                                                                                                                                                                                                453
                                                                                                                                                                                                TVGKSSSTAYMELRSLTSEDSAVYFC-----ARRRIAYGY---DEGHAMDYWGQGTSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ce represents the heavy chain variable region F19 antibody (chF19HC). F19 (ATCC Accession r
                                                                                                                                                                                                                                                                                                                               Conservative
                      - PELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
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Pred. No. 1e-62;
                                                                                                TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-
                                                                                                                                                                                                                                                                                                                               Mismatches
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lamed skin.
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KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ

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RESULT 74
ABG31025
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that is capable of at least one immunological activity, compribinding domain polypeptide fused to an immunoslobulin hinge repolypeptide capable of specifically binding to an antigen, or immunoslobulin heavy chain CH2 or CH3 constant region polypept to the hinge region polypeptide or to the CH2 constant region
                                                                                                                                            New human binding domain-immunoglobulin fusion protein useful for treating a subject having or suspected of having a B-cell disorde malignant condition e.g. rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Synthetic.
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                                                                                   The invention
                                                                                                                 Disclosure;
                                                                                                                                                                                                                                                               Ledbetter JA,
                                                                                                                                                                                                                                                                                                                             17-JAN-2001; 2001US-00765208
                                                                                                                                                                                                                                                                                                                                                           17-JAN-2002; 2002WO-US001487
                                                                                                                                                                                                                                                                                                                                                                                                                          WO200256910-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse/human chimeric fusion protein
                                                                                                                   Page 120-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                describes a binding domain-immunoglobulin fusion prole of at least one immunological activity, comprising n polypeptide fused to an immunoglobulin hinge region
                                                                                                                                                                                                                                                               Hayden-Ledbetter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment
266. .499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Mouse anti-human
fragment (scfv)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Human immunoglobulinG1 (IgG1)
fragment of crystallisation, CH2 and (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
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     or CH3 constant region polypeptide or to the CH2 constant region
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CH3 do
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domains"
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RESULT 75
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ID ADD25
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DT 15-UP
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DE Bindi
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XW Bindi
KW antie

(first

entry)

ADD25587

standard;

protein; 499

Binding

domain-immunoglobulin fusion protein-associated protein

Binding domain; immunoglobulin; fu antiarthritic; immunosuppressive;

immunoglobulin; fusion

usion protein; antidiabetic;

cytostatic; antithyroid;

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide. The fusion protein is useful for treating a subject having or suspected of having a B-cell disorder or malignant condition e.g. rheumatoid arthritis, myasthenia gravis, Grave's disease, Hashimoto's thyroiditis, type I diabetes mellitus, multiple sclerosis, systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 499
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                         LSLSPG
                                                                                                                                                                                                                                                                                                                                                                               GAIYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOGNKYVLGKKGDTVELTCTASOKKSIOFHWKNSNOIKILGNOGSFLTKGPSKLNDRADS
LSLSPG
                                                                       WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                 WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                                                                   CKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVE
                                                                                                                                                                         CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE
                                                                                                                                                                                                                             CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK
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                                                                                                                                                                                                                                                                                                     FDVWGTGTTVTVSDQEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVT
                                                                                                                                                                                                                                                                                                                                           IDI-----VPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVT
                                                                                                                                                                                                                                                                                                                                                                                                                       ------GKNIQGGKTLSV------SQLELQDSGTWTCTVLQNQKKVEFK
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comprising a binding domain polypeptide, an immunoglobulin fusion protein CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CC CH2 constant region polypeptide that is fused to the CH2 constant region polypeptide, and an immunoglobulin heavy chain CC polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide, derived from (a) having 3 or more region polypeptide, derived from (a) having 3 or more cysteine is mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine is not mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine is not mutated, a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine is not mutated, a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (c) having 3 or more cysteine residues; where cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one cysteine residue; where constitute the cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains or polypeptide, derived from (c) having 3 or more cysteine residues; where constitute the service of immunoglobulin hinge region polypeptide contains or ocysteine residues. The binding domain-immunoglobulin fusion protein is capable of at least one immunoglobulin hinge region polypeptide contains or comparising the polypucleotide doplymucleotide encoding the binding domain-immunoglobulin fusion protein, a recombinant expression construct comprising the polypucleotide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a protein or polypucleotide are an isolated polymucleotide in a binding domain-immunoglobulin fusion protein, a protein or polymucleotide and a carrier, and treating a subject construct of the binding domain-immunoglobulin fus
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17-JAN-2002;
03-JUN-2002;
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having or suspected of having a malignant condition or a B-cell
r, e.g. melanoma, Grave's disease or autoimmune disease.
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2002US-00053530
2002US-0385691P
sequences in the printed specification by their SEQ ID re none of the sequences can be explicitly their SEQ ID
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Best Local
             17-JAN-2001; 2001US-0367358P
17-JAN-2002; 2002US-00053530
03-JUN-2002; 2002US-0385691P
                                                                                                                                                                                                                                 Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
                                                                                                                                                                                        malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                     26-JUN-2003
                                                                                                                                                                                                                                                                                                                          Binding
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                                                                                                                                                                                                                                                                                                                                                                                                                ADD25454 standard; protein;
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                                                                                                                                                            Unidentified
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t; Pred. No. 1.1e
27; Mismatches
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1.1e-62;
hes 93;
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification and is also available in electronic format directly from USPTO at sequence.html?DocID=20030118592. The authors have not identified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide. The polypeptide that is fused to the CH2 constant region polypeptide. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, myasthenia gravis, Grave's disease, type I diabetes mellicus, multiple sclerosis or autoimmune disease. The present sequence is a binding doma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                             RFSGSGSGTSYSLTISRVEAEDAATYYC----QQWSFNPPTFGAGTKLELKDGGGSGGGG
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                                                                                                                                                                                                                                                                                                                           TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS
                                                                                                                         ---TANSDTHLLQ-GOSLTLTLESPPGSSPSVQCR---
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---GKNIQGGKTLSV------SQLELQDSGTWTCTVLQNQKKVEFK 196
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Pred. No. 1.1e-62;
7; Mismatches 93;
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N-PSDB; ABZ24633, AE
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New humanized forms of mouse 3D6 antibodies, useful for treating Down's

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Best Local :
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Matches 270
                                                                                                                                                                                                                                                            The human monoclonal antibody D7C2, of isotype IgM, recognises a 30-32 kD polypeptide on the membrane of rhesus positive red blood cells. The antibody agglutinates rhesus positive cells but not rhesus negative cells and is useful diagnostically and also for preventing haemolysis in newborn rhesus positive babies. Recombinant IgM-D7C2 can be produced by insect cells which have been transformed by a baculoviral vector comprising a D7C2 expression cassette. The present sequence is that of a recombinant IgM-D7C2 heavy chain fused downstream of a mouse VH signal
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                                                                                                                                                          KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQ--GSFLTKGPSKLNDRADSRRSL---
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variable region from a
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rhesus negative; haemolysis; gamma 1 heavy chain;
insect host cell; baculovirus; recombinant productio
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                                                2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and heavy variable genes (see also AAT62512 and AAT62513) are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of the primatised antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1 antibodies have also been produced (see also AAW01817-20). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders and graft-versus-host disease. (Updated on 17-OC7-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Monkey monoclonal antibody binding human for treating auto:immune disease or graft
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-human B7.1 antigen antibody 16C10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody;
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cynomolgus monkey; macaque; 16C10;
B7 antigen; CD28; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanna
                                                                                                                                                                                                                                                                                                                                                                                       English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             human B7.1 or B7.2 antigen -
graft-versus-host disease.
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Sequence 476

New monoclonal antibodies specific inhibiting binding to CD28 - useful

for las

B7.1 or B7.2 antigens and specific immunosuppressants

for

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RESULT 80
AAW63765
ID AAW63
XX AA63
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XW CD86;
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Best Local Similarity
Matches 274; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD86; inhibitor; immunosuppressant; T cell/B cell interaction; tumour; immunogen; anti-idiotype reagent; if
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; (CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; Teal/B cell interaction; tumour; inflammation; imaging agent; varimmunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobul:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW63765 standard;
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DB; AAV35489.
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59.8%;
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Pred. No. 1.2e-62;
9; Mismatches 87;
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IgG; immunoglobulin G;
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RESULT 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a primatized form of the antibody 16C10 heavy chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (MAb's) that bind selectively to 87.1 (CD80) or to 87.2 (CD80) antigens and inhibits binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I dispathic thrombocytopaenia purpura, systemic lupus erythematosus, type inflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAb can be conjugated to a drug or toxin. MAb's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop antidiotype reagents. MAb's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunoglobulin G (IgG) responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 274
                Protein sequence
                                                       12-MAR-2002
                                                                                                                         AAU11646
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                                                                                                                                                                                                                                KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                     YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                                                                                                                                                                                                                                             TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                                                                                                                                                                                                                                                             CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGKKGDTVELTCTASQ---KKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            476 AA;
                                                                                                                                                                                                                                                                                                                                                       TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                                                                                                                                                                                                                                                                             ---PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QDSG-----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS------QLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISTDTSKNQFSLKLNSMTAADTAVYYC-VRDRLFSVVGMVY-----NNWFDVWGPGVLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTYYNPSLKSQVT
                                                                                                                                                                                                               KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                   YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPP
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                                                     (first entry)
                of primatised
                                                                                                                         protein;
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59.8%;
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Pred. No. 1.2e-62;
9; Mismatches 87;
                    form
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ff
                  the heavy chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                  of 16C10 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B cells,
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Best Local S
Matches 274
                                                                                                                                                                                                                                                                                                                                                                 purpura, systemic lupus, erythematosus, type 1 diabetes mellitus, renumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating proliferative and hyperproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative colitis, food-related allergies e.g. migraine, rhinitis and eczema, and other types of allergies. The present protein sequence represents the heavy chain of 16C10, a primatised antibody used in the invention to induce apoptosis and inhibit production of interleukin-2 (IL-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD86) for inducing the apoptosis of B7+ cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leukaemia, and autoimmune diseases such as idiopathic thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of monoclonal antibody which specifically binds to B7 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cecancer, graft-vs-host disease and autoimmune disease such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; macaque monkey; light chain; primatised antibody; 16C10 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7_1 antigen; CD80; B7_2 antigen; CD86; B cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; cell lymphoma; B cell leukaemia; autoimmune disease; inmunosuppression; organ rejection; interleukin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                  Sequence 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 8; Fig 5b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
Macaca sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAY-2001; 2001WO-US016364.
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DB; AAS17247.
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                                                                                                                                                                                                                      30 LGKKGDTVELTCTASQ----KKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRS
                                                                                                                                                                                                                                                                                Similarity
                                                                            LESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS
                                                                                                                                                  L---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT
         QDSG--
                                             VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
                                                                                                                                                                                        LVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLEWIGSFYSSSGNTYYNPSLKSQVT
                                                                                                                ISTDTSKNQFSLKLNSMTAADTAVYYC-VRDRLFSVVGMVY----NNWFDVWGPGVLVT
                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                            47.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brams
                                                                                                                                                                                                                                                           29;
                                                                                                                                                                                                                                                                            Score 1271;
Pred. No. 1
       ---TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      שי
                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                            DB 5;
                                                                                                                                                                                                                                                             87;
                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                             Indels
                                                                              ----QLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B7.1 antigen CD cells, treating
                                                                                                                                                                                                                                                                                                 476;
                                                                                                                                                                                                                                                             68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      allergy.
                                                                                                                                                                                                                                                             Gaps
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       216
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QSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKAEPKSCDKTHTCPP

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RESULT 82
ADD25787
ID ADD25
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The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide that is fused to the CH2 constant region polypeptide. The hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide.
                                                                                                                                                                                                                                                                                         New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JAN-2001; 2001US-0367358P
17-JAN-2002; 2002US-00053530
03-JUN-2002; 2002US-0385691P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation; malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;
                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 348; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rheumatoid arthritis; myasthenia gravis; Grave's disease;
type I diabetes mellitus; multiple sclerosis; autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroprotective; hing CH2 constant region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Binding domain; immunoglobulin; fusion protein; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD25787
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-801317/75
                                                                                                                                                                                                                                                                                                                                                                                                         Ledbetter JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUL-2002; 2002US-00207655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003118592-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiarthritic; immunosuppressive; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD25787 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENECRAFT INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                         Hayden-Ledbetter MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hinge region; immunoglobulin heavy
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                                                                                                                                                                                                                                                                                                                                                                                                       Thompson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chain;
                                                                                                immunoglobulin
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CC (a) having 3 or more cysteine residues, where the mutated human IgG1 cimmunoglobulin hinge region polypeptide contains no more than one CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge region CC polypeptide, derived from (a) having 3 or more cysteine residues; where CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains CC capable of at least one immunological activity comprising antibody CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The CC binding domain polypeptide is capable of specifically binding the construct comprising the polypucleotide of specifically binding the construct comprising the polypucleotide (operably linked to a promoter), a host cell transformed or transferted with a recombinant expression CC construct, producing the binding domain-immunoglobulin fusion protein, a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a construct, producing the binding domain-immunoglobulin fusion protein, a construct, producing the binding domain-immunoglobulin fusion protein, a construct, producing the binding domain-immunoglobulin fusion protein, a comprising the binding domain-immunoglobulin fusion protein, a compart of having a malignant condition or a B-cell disorder. CC thaving or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis, compasthenia gravis, Grave's disease, type I diabetes mellitus, multiple consumber therefore autoimmune disease. The present sequence is a binding domain immunoglobulin fusion protein-associated protein sequence. Note: The sequence data for this patent formed part of the printed specification comprised specification or compasted the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.

XX sequence 504 AA;
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Ś á á 밁 Ś 밁 Ś 밁 S 밁 5 Ş 밁 밁 밁 Query Match
Best Local Similarity
Matches 282; Conser 171 471 411 339 351 279 291 219 231 174 154 113 99 8 19 Н QIKILGNQGSFLTKGPSKLNDRADSRRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKE LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE -- QGNTLPWTFGGGTKLVTKRELGGGGSGGGGGGGGGGGGGTDEVQLQQSGPELVKPGASMSC 170 TVKLL----IYYT---SRLHSGVPSRFSGSGSGTDYSLTIANLQPEDIATYFCQ-----MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHW---KNSN KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD EQYNSTYRVV\$VLTVLHQDWLNGKEYKCKV\$NKALPAPIEKTISKAKGQPREPQVYTLPP LLSLTSEDSAVYYCARSGYYGDSDWYFDVWGAGTTVTVSSDQEPKSCDKTHTCPPCPAPE ---LELQDSGTWTCTVLQNQKKVEFKID-----IVPCPAPEPKSCDKTHTC----PE KASGYSFTGYIVNWLKQSHGKNLEWIGLINPYKGLTTYNQKFKGKATLTVDKSSSTAYME EVOLLVFGLTANSDTHLLQGQSL------TLTLESP----PGSSPSV 153 MSRGVDIQ------MTQTTSSLSASLGDRVTISCRASQDIRNYLNWYQQKPDG KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG SRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVD EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPRE Conservative -----RSPRGKNIQ--------GGKTLSVSQ-----47.0%; Score 1271; DB 7; 55.0%; Pred. No. 1.2e-62; tive 29; Mismatches 92 92; Length 504; Indels 110; Gape 112 173 65 410 338 350 290 218 470 398 278 13

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                                                                          The present sequence is the protein sequence of the heavy chain of a chumanised antibody of the present invention. In the variable portion, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 10D5 and the framework region originates from human germine VH segment DP-28 and J segment JH4. Novel humanised antibodies of the invention have CDRs from 10D5 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope contained antibodies have binding affinities (affinity and epitope contained antibodies have binding affinities, the mouse 10D5 antibody. The invention includes antibodies, single chain antibodies, and their contained antibodies, and their contained antibodies antibody to treat, prevent, and methods of using the humanised antibody to treat, prevent, associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New humanized 10D5 antibody, useful for the manufacture of a medicament for treating Down's syndrome, clinical or pre-clinical Alzheimer's disease or cerebral amyloid angiopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-183836/18.
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                                                            reduce Abeta plaque
OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 13-15; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vasquez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001US-0287653P
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(first entry)
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/note= "CDR2"
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manised antibody; antibody; Alzheimer's disease;
cerebral amyloid angiopathy; neuroprotective; nootropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Sequence

472

New human type complementation-determining region-transplanted antibody and derivatives against ganglioside GD3, useful in diagnosis and therapy of e.g. tumors, with low antigenicity, little side effects but potent

Claim 41;

Page 168-172; 183pp; Japanese

activity in cancer.

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RESULT 84
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                                                                                                                              30-SEP-1999; 99JP-00278291
06-APR-2000; 2000JP-00105088
                                                                                                                                                                                                                                          Ganglioside; cancer.
                                                                                                                                                                                                                                                                       Ganglioside
                                                                                       Hanai N,
                                                                                                                                                           29-SEP-2000; 2000WO-JP006774
                                                                                                                                                                                05-APR-2001
                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                           03-JUL-2001
                                                                                                                                                                                                                                                                                                                AAB81987;
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                                                                    WPI; 2001-266143/27
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                                                                                                          KYOWA HAKKO
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                                                                                                                                                                                                                                                                                                                                                                                                 ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSVS-----QLELQDSG-----
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                                                                                      Shitara K,
                                                                                                                                                                                                                                                                        GD3
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                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                       specific antibody related protein SEQ ID NO:
                                                                                                           Kogyo
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                                                                                        Nakamura
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Mismatches
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                                                                                                                                                                                                                                                   region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----TWTCTVLQNQKKVEFKI
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Best Local S
Matches 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a monoclonal antibody which can react specifically with ganglioside GD3. The antibody and its derivatives are useful in the diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention
                                                                                                                                                                       Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma; immune system disease; leukaemia; allergy; inflammatory disease; tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease; psoriasis; rheumatoid arthritis; conjunctivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                           21-JUL-2000; 2000US-0220139P
                                                     20-JUL-2001; 2001WO-US023082
                                                                                                         WO200208257-A2
                                                                                                                                                                                                                                         Siglec-BMS-L3a-hIg
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  (BRIM ) BRISTOL-MYERS SQUIBB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                G-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                        QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KALPAPIEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGSGTYYSDSVKGRFTIS-RDNSKNTLY-----LQMRSLRAEDSAVYFC----TRVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNQGSFLT---KGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  582 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVD----KKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTLSVS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGTYYFDS-----WGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
                                                                                                                                                                                                                                                                                                                                                                                     GKAPTSSSTKKTQLQLEHLLLDLQ
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                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                       fusion
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                                                                                                                                                                                                                                         protein
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Pred. No. 1.6e
26; Mismatches
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                                                                                                                                                                                                                                       (Siglec-BMS-L3a-hIg).
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CC are useful for treating immune system diseases such as asthma, leukaemia are or their allergic or inflammatory diseases. Extracellular domains of (I) crepresent potential markers for screening, diagnosis, prognosis, follow-cc inhibit inflammation, tissue damage and remodeling in asthma, and cc inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's cd disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is cc disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is cc also useful for monitoring the course of disease or disorders, and for cl dentifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are useful in diagnosis and/or prognosis methods, and to detect the presence cc and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS proteins in a biological sample. (II) are useful as nucleic acid probes care useful for screening genomic library to isolate a genomic clone of SIGLEC gene. SIGLEC-BMS gene copy number is determined for detecting cd iseases or disorders associated with SIGLEC-BMS transcripts or proteins. The sIGLEC-BMS artibodies are also used to detect, sort or isolate cells expressing SIGLEC-BMS proteins and in diagnostic imaging technology. Calcium the college of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 11; Fig 23; 209pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Longphre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               related lectin)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 an isolated SIGLEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pharmaceutical compositions compris-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (sialic acid-binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease
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Query Match Best Local S Matches 273 Sequence Similarity B 47.0%; Score 1270; DB 5; Pred. No. 1.7e-62; 7; Mismatches 90 Length 619;

619

á 밁 S 밁 밁 S 밁 밁 S 밁 á S 447 387 331 158 181 260 205 273; 64 œ -----KEEVQLLVF-----GLTANSDTHLLQGQSLTL---TLESPPGSSPSVQCRS RHLLLVLQLALLPA---ATQGNKVVL-GKKGDTVELTCTASQKKSIQFHWKNSNQIKILG PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK -RLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSV---HD LSVQYPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPA------NQGSFLTKGPSKLNDRADSRRSLWDQGNFPL1IKNLKIEDSDTYICEVEDQ------RDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSW------PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK PEPKSCOKTHTCPPCPAPEFEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK PRGKNIQGGKTLSVSQ------LELQDSGTWTCTVLQ--NQKKVEFKIDIVPCPA Conservative ---VLQNRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALD VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 27; 90; Indels 82; 618 431 Gaps 319 204 157 279 230 63 379 506 446 259 386 330 114 11;

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ABB99224
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                                                                                                 Query Match
Best Local S
Matches 275
                                                                                                                                                                         The invention relates to a novel binding molecule comprising at least one antigen binding site comprising in sequence the hypervariable regions CDR1, CDR2 and CDR3. The molecule of the invention has immunosuppressive, antipsoriatic, antiinflammatory, and antiallergic activity. The molecule of the invention is a CD45-Antagonist. The binding molecule or humanised antibody is useful as a pharmaceutical in the treatment of autoimmune diseases, transplant rejection, psoriasis, inflammatory bowel disease and allergies. The binding molecule has a binding specificity for both CD45RO and CD45RB in medicine, where the binding molecule is a chimeric, a humanised or a fully human monoclomal antibody. The sequence represents the heavy chain of the CD45RO/RB binding molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aversa G,
Saldanha
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 31; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        New binding molecule having at least one antigen binding site, useful a pharmaceutical in the treatment of autoimmune diseases, transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-723357/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-FEB-2001; 2001GB-00003389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-FEB-2002;
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunosuppressive; antipsoriatic; ant CD45-Antagonist; autoimmune disease; inflammatory bowel disease; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB99224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric
                                                                                                                                                                                                                                                                                                                                                                           rejection, psoriasis, inflammatory bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200272832-A2
                                          11
                 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD45; CD45RO; CD45RB; binding molecule; CDR1; CDR2; CDR3; suppressive; antiapsoriatic; antiinflammatory; antiallergic;
                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOVARTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             JW.
ADSRRSLW----DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG
                                                                                                                                                     448 AA;
                                         LVKPGASVKMSCKASGYTFTNYIIHWVKQEPGQGLEWIGYFNPYNHG-----TKYNEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD45RO/RB
                                                                    LGKKGDTVELTCTASQKKSIQF--HW---KNSNQIKILG----NQGSFLTKGPSKLNDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kolbinger F,
1, Hall BM;
                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50. .66
/label= CDR2
99. .107
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= CDR1
50..66
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                                                                                                           47.0%;
59.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carballido Herrera
                                                                                               27;
                                                                                              Score 1269.5; DB 5;
Pred. No. 1.3e-62;
7; Mismatches 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transplant rejection; psoriasis; heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                           and allergies
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                                                                                               Indels
                                                                                                                         Length 448;
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RESULT 87
AAY94AB
ID AAY9
XX AAY9
XX AAY9
XX DT 11-S
XX Huma
XX Huma
XX Huma
XX Homo
OS Homo
OS Homo
OS Homo
OS Homo
XX WO20
PN WO20
PN WO20
PN WO20
PF 02-D
XX WF1;
DR N-S3
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N-PSDB; AAA30442.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cellular adhesion molecule; ACAM; nootropic; antiepileptic;
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The present sequence is a fusion protein comprising part of human VCAM-1 and the Fc region of human IgGI. The sequence encoding this protein was generated by integrating the VCAM-1 coding region into a plasmid designated pDEF24/IgGI, which encodes the hinge and constant CH2-CH3 domains of human IgGI. The sequence was then ligated to the expression vector pDEF24 and transformed into DH5a competent cells. The fusion protein was used as a control in adhesion experiments involving ACAM#4/IgG-Fc and ACAM#6/IgG4-Fc fusion proteins. ACAM#4 and ACAM#6 are

Nucleic acids encoding ACAM, a human cellular adhesion molecule, for diagnosing, preventing and treating diseases associated with expression and activity, e.g. epilepsy and schizophrenia.

Example 5; Page 174-176; 187pp; English:

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RESULT 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            change foetal brain cDNA clones containing alternatively spliced full-
clength variants of a novel adhesion molecule designated ACAM. ACAM
culcic acids and polypeptides may be used in the prevention, treatment
and diagnosis of diseases associated with inappropriate ACAM expression
and activity such as dementia, epilepsy, schizophrenia, peripheral nerve
clinjuries and diabetic neuropathies. They may be used to rectify mutations
or deletions in a patient's genome that affect the activity of ACAM or to
supplement insufficient ACAM production in a patient. Conversely,
antisense nucleic acid molecules may be administered to down-regulate
ACAM expression. The nuclectide sequence may also be used as a DNA probe
in diagnostic assays (e.g. PCR) to detect and quantitate the presence of
similar nucleic acid sequences in samples, and hence determine which
patients may be in need of restorative therapy. ACAM polypeptides may be
used as antigens in the production of antibodies against ACAM and in
assays to identify modulators (agonists and antagonists) of ACAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 264; Conserv
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Best Local :
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                                 Homo sapiens
                                                    Synthetic.
                                                                                    antiarthritic;
                                                                                                      CD19;
                                                                                                                                      CD19:zeta chimeric
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                                                                                                      chimeric;
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                                                                                                                                                                                                                                                                                                                                           GNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            744 AA;
                                                                                                                                                                                                                                        standard; protein; 634 AA
                                                                                                                                                                                                                                                                                                                                                                                            KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
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                                                                                                                                                                                                                                                                                                                           GNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                     (first entry)
                                                                                  antiinflammatory; gene therapy; CD8; immunosuppressiv
Location/Qualifiers
                                                                                                                                      immunoreceptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.0%;
59.1%;
                                                                                                      CD19R:zeta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1269.5; DB 3;
Pred. No. 2.3e-62;
8; Mismatches 65;
                                                                                                                                                                                                                                                                                                                           743
                                                                                                                                                                                                                                                                                                                                                             431
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                                                                                                    immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to genetically engineered CD19-specific immune cells which express, and bear on the cell surface membrane, a CD19-specific chimeric receptor. The CD19-specific chimeric T cell receptor consists of: (a) an intracellular signaling domain selected from zeta, et and FcepsilonRI, for an effector function of the immune cell; (b) at least 1 transmembrane domain and (c) at least 1 extracellular domain comprising a CD19-specific receptor. The compositions and methods of the malignancies and for abrogating any untoward B cell function in autoimmune disorders such as lupus or rheumatoid arthritis. The present sequence represents a CD19:zeta chimeric immunoreceptor amino acid sequence. This chimeric receptor was constructed by PCR splice overlap extension and consists of human GM-CSF receptor alpha chain leader peptide, FM63 Vh, Gly-Ser linker, FM63 Vl, human IgG1 FC, human CD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 287; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 634 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetically engineered CD19-specific immune cells, useful for cellular immunotherapy of CD19 malignancies and for abrogating any untoward B continuation in autoimmune disorders such as lupus or rheumatoid arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-2000; 2000US-0246117P
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                                                                                                                                                                                                                                                                                                              QKE----EVQLLVFGLTANSDTHLLQGQSLT----LTLESPPG-----SSPSVQC----
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YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                        GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                           GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                    VSLPDYGVSWIRQPPRKGLEWLGVIWGSETTYYNSALKSRLTIIKDNSKSQVFLKMNSLQ
                                                                                                                              TDDTAIYYCA----KHYYYGGSYAMDYWGQGTSVTVSSVEPKSSDKTHTCPPCPAPELL
                                                                                                                                                                LQDSGTWTCTVLQNQKKV----EFKIDI-----VPCPAPEPKSCDKTHTC-----PELL
                                                                                                                                                                                                                                                                            TLPYTFGGGTKLEITGSTSGSGKP-GSGEGSTKGEVKLQESGPGLVAPSQSLSVTCTVSG 173
                                                                                                                                                                                                                                                                                                                                                                                                                        LLLVTSLLLCELPHPAFLLIPDIQMTQTTSSLSASLGDRVTISCRASQDISKYLNWYQQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain
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                                                                                                                                                                                                                                        ----RSPRGKNIQ-----GGKT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.9%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and human cytoplasmic zeta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1268; DB 6;
Pred. No. 2.3e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94;
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eta chain
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                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                 The invention relates to treating cognitive symptoms or reducing disease progression in a subject having a condition or disease associated with amyloid-beta peptide (Abeta). The method involves administering an amount of an anti-Abeta antibody that has greater affinity for soluble Abeta than 10^-9 M, that has affinity (KD) for soluble Abeta-40 or Abetal-42 higher than 10^-9 M, or that has greater affinity for soluble Abeta than antibody 266 has. The method or the anti-Abeta antibody is useful in preparing a medicament for treating cognitive symptoms or reducing disease progression in a subject having a condition or disease associated with Abeta. The condition or disease is Alzheimer's disease, Down's syndrome, cerebral amyloid angiopathy, vascular dementia, or mild cognitive impairment. The present sequence represents a humanised anti-Abeta antibody 266 heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating or reducing the progression of diseases associated with amyloid-beta peptide, e.g. Alzheimer's disease, vascular dementia or mild cognitive impairment, comprises administering an anti-amyloid-beta
                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide antibody.
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28-MAY-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amyloid-beta; Abeta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanised anti-Abeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR39465
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                                                                                                                                                                           274;
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        77
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                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                        442 AA;
NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG
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                                                           LVQPGGSLRLSCAASGFTFSRYSMSWVRQAPGKGLELVAQINSVGNSTYYPDTVKGRFTI
                                                                                                             LGKKGDTVELTCTAS--QKKSIQFHWKNS------NQIKILGNQGSF--LTKGPSKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page
                                                                                                                                                                           Conservative
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2002US-0383851P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-22; 84pp; English.
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Pred. No. 1.7e-62;
6; Mismatches 69
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The present invention relates to a method for effecting rapid improvement of cognition in a subject having a condition or disease related to the Abeta peptide. The method comprises administering an anti-Abeta antibody. The method is useful for treating cognitive impairments associated with Abeta peptide including those involved in Alzheimer's disease, Down's

improvement

Effecting rapid improvement of cognition in a subject having Alzheimer' disease, Down's syndrome, cerebral amyloid angiopathy, or mild cognitivimpairment, comprises administering anti-A beta antibody.

lzheimer's

Disclosure;

Page 21-23; 85pp;

English

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RESULT 90
ABU08311
                                                                                                                                                                                                                                                                                                                                               Mouse; cognition; Abeta peptide associated disorder; anti-Abeta antibody; cognitive impairment; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; vascular dementia; nootropic; neurotropic; mild cognitive impairment; antibody 266; heavy chain; humanised; mutant;
                                                                                                                                                                                                                                                                                           Mus
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                                  Bales
                                                                                                        17-AUG-2001; 2001US-0313222P.
28-MAY-2002; 2002US-0383846P.
                                                                                                                                                             14-AUG-2002; 2002WO-US021323.
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Best Local
17-AUG-2001;
17-AUG-2001;
23-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                Complementarity determining region; CDR; humanised; mouse; heavy; variable; domain; antibody; preclinical; clinical; Alzheimer's disease; epitope; amyloid beta peptide; Abeta;
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                                                                                                                                                                    27-FEB-2003
                                                                                                                                                                                                                       WO2003015617-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVQPGGSLRLSCAASGFTFSRYSMSWVRQAPGKGLELVAQINSVGNSTYYPDTVKGRFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS------
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2001US-0313221P.
2001US-0313224P.
2001US-0334987P.
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Pred. No. 1.7e-62;
6; Mismatches 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           266;
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05-NOV-2002 ABB81109

(first entry

ABB81109

standard;

protein;

Anti-tissue factor (TF) heavy chain fragment

Immunoglobulin; promoter; cytostatic; antiinflammatory; immunomodulator;

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RESULT 92
ABB81109
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AC ABB81
AC ABB81
XX
DT 05-NC
XX
DE Anti-
XX
Immur
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Best Local S
Matches 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences given in AAG90104-09 represent preferred antibodies of th invention. This sequence represents the preferred heavy chain. The humanised antibody of the invention may be used for diagnosing preclinical or clinical Alzheimer's disease. The antibody specifically binds an epitope, preferably the amyloid beta peptide (Abeta). The antibodies sequester Abeta from its bound, circulating form in blood an alter clearance of soluble and bound forms of Abeta in central nervous system and plasma. The antibodies specifically bind an epitope representing amino acids 13-28 of the Abeta molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosing preclinical administering an antibo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 442 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 15-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 LGKKGDTVELTCTAS--QKKSIQFHWKNS------NQIKILGNQGSF--LTKGPSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                     TFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDK
                                                                                                                                                                                       SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                 --QLELQDSG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG
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                                                                                                                                                                                                                                          PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
                                                                                                                                                                                                                                                                                                EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                          QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSLTLTLESPPGSSPSVQCRSPRGKNIQGG-----KTLSVS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-RDNAKNTLYLQMN-----SLRAEDTAVYYC-------ASGD---YWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVQPGGSLRLSCAASGFTFSRYSMSWVRQAPGKGLELVAQINSVGNSTYYPDTVKGRFTI
                                                                                                                                                                        SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                             PREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDG
                                                                                                                                                                                                                                                                                EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eclinical or clinical Alzheimer's disease an antibody which specifically binds an
                                                                                                                                                                                                                                                                                                                                                  - PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
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59.1%;
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Pred. No. 1.7e.
26; Mismatches
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.7e-62;
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blood and
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                                                                                                                                                                                                                                                                                                                                                           the first promoter-cistron pair comprises a first translational
cintilation region (TIR-L) operably linked to a nucleic acid sequence
encoding an Ig light chain and the second cistron of the second promoter-
cistron pair comprises a second translational initiation region (TIR-H)
coperably linked to a nucleic acid sequence encoding an Ig heavy chain.
Upon expression of the polynucleotide in a prokaryotic host cell, light
and heavy chains are folded and assembled to form a biologically active
If The antibody of the invention is useful for diagnosing, treating or
preventing diseases or conditions associated with abnormal expression and
/or activity of one or more antigen molecules e.g. lymphoid malignancies,
inflammatory, anglogenic, immunologic, neuronal, glial, astrocytal,
hypothalamic or other glandular disorders. The present sequence
crepresents the amino acid sequence of an anti-tissue factor (TP) heavy
chain fragment of the cistron vector paTF50
                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 275
                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide comprising first and second promoter-cistron pairs, useful for diagnosing, treating or preventing diseases associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Ig), comprising a first or second promoter-cistron pair consisting first or second promoter and cistron, respectively. The first cistrone first promoter-cistron pair comprises a first translational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides a polynucleotide, which encodes an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200261090-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuroprotective;
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                                                                                                                                                                                                                                                                                Similarity
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SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPK
                                                                                                -LQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG------KTLSVS-----
                                                                                                                               TISADNSKNTAYLOMN-----SLRAEDTAVYYCA----
                                                                                                                                                                ---- DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL--
                                                                                                                                                                                               LVQPGGSLRLSCAASGFNIKEYYMHWVRQAPGKGLEWVGLIDPEQGN--TIYDPKFQDRA
                                                                                                                                                                                                                                LGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKILG-NQGSFLTKGPSKLNDRA
                               -----QLELQDSG-------TWTCTVLQNQKKVEFKIDIVPCPAPEPK
                                                               DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig 20A-C; 104pp; English.
                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                46.9%;
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                                                                                                                                                                                                                                                               Score 1266; DB 5;
Pred. No. 2.2e-62;
6; Mismatches 69;
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RESULT 93
ABP72748
AID 72478
AID ABP7
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The present sequence is that of an anti-tissue factor (TF) antibody heavy chain including a heat stable enterocoxin II (STII) secretion signal. This recombinant heavy chain is produced by host cells transformed with claimed vector pxTF-7T3FL (see ABZ82072). The plasmid contains 2 translational units that temporally separate the transcription of the antibody light (see ABP72747) and heavy chains. Expression of the light chain is under the control of the phoA promoter, while expression of the heavy chain is under the control of the inducible TacII promoter. In an example from the invention, Escherichia coli 60H4 was transformed with pxTF-7T3FL. The light chain was expressed initially and secreted into the periplasmic space. Heavy chain production was then induced by addition of IPTG A yield of 2.6 +/- 0.3 g/l assembled F(ab')2 was obtained, compared
                                                                                                                                                                                                                                                                                                                                                                         Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody; heavy chain;
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                                                                                                                                                                                                                                                                                                                                                                                                                       an antibody for treating cancer or autoimmune diseases the host cell under suitable conditions so that the light chain are expressed in a sequential fashion.
                                                                                                                                                                                                                                                                                                                                                                       Fig 10; 73pp;
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                                                                                                                                                                                      human rabies-immune globulin; monoclonal; virucide; heavy chain; monoclonal rabies virus neutralising antibody; immunoglobulin; chain; central nervous system; CNS; prophylactic therapy; clone JA.
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                                                                                                                                                                                                                                                                                                                                                                                                                 DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----QLELQDSG-------TWTCTVLQNQXKVEFKIDIVPCPAPEPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVQPGGSLRLSCAASGFNIKEYYMHWVRQAPGKGLEWVGLIDPEQGN--TIYDPKFQDRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---- DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL--
                                                                                                                                                                                                                                                  protein of the monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                     2001WO-US014468
                                                                                                                                                                                                                                                                               (first entry)
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; Pred. No. 2.2e-62;
26; Mismatches 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 470;
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RESULT 95 ABU08017 ID ABU08

standard;

protein;

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BXGXAX

10-MAY-2003

(first entry)

ABU08017;

Human monoclonal rabies virus antibody heavy chain,

clone JH,

protein.

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Matches 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated human monoclonal rabies virus neutralizing antibody useful for treating individual exposed to rabies virus and for preventing spread
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427
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                                                                                                                                                                        DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                                                                                                                               CDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                                                                                                                                                                                                                                                                                                                                                YWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL 133
                       SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
                                                                                                                                                                                                                           CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                                                                                                                                                                                                                                                                      GVHTFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKS
SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                         KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
                                                                                                                                                  DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1266; DB 5;
Pred. No. 2.2e-62;
2; Mismatches 71;
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The invention discloses a recombinant antibody comprising a constant region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable region. Rabies is an acute, neurological disease caused by infection of the central nervous system with the rabies virus, a member of the Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods for producing an isolated recombinant antibody by culturing a host cell, containing a recombinant expression vector comprising the nucleic acid molecule encoding the antibody, and isolating the recombinant antibody expressed and treating an individual exposed to a pathogen by administering to the individual the recombinant antibody. The recombinant expressed to a pathogen, e.g. rabies infection. They are also useful for the sequences presented are the antibody protein fragments, the nucleic acids encoding them or the PCR primers used to construct the recombinant
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Best Local S
Matches 276
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les 276; Conserv
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DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                 CDXTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                                                                                                                               GVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KRVEPKS
                                                                                                                                                                                                                                                                          YWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL
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                                                    CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
                                                                                                                                                                                                                      ----QLELQDSG----
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Pred. No. 2.2e-62;
2; Mismatches 71;
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17-JAN-2002; 2002US-00053530
03-JUN-2002; 2002US-0385691P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
                                                                                                                                                                                                                                                                                      Ledbetter JA, Hayden-Ledbetter MS,
                                                                                                                                                                                                                                                                                                                                                                          25-JUL-2002; 2002US-00207655
                                                                                                                                                                                                                                                                                                                                                                                               26-JUN-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             mellitus; multiple sclerosis; autoimmune disease
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The invention relates to a binding domain-immunoglobulin fusion protein CC comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CC immunoglobulin hinge region polypeptide that is fused to the hinge region CC polypeptide, and an immunoglobulin heavy chain CH3 constant region CC polypeptide, and an immunoglobulin heavy chain CH3 constant region CC polypeptide that is fused to the CH2 constant region polypeptide. The hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; contains 2 cysteine residues, where the first cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine is not mutated; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (b) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (c) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (b) having 3 or more cysteine residues. The binding domain-immunoglobulin fusion protein is New binding domain-immunoglobulin fusion protein, useful for treating subject having or suspected of having a malignant condition or a B-cel disorder, e.g. melanoma, Grave's disease or autoimmune disease. Disclosure; SEQ ID NO 398; 157pp; English. ating a B-cell

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dependent cell-mediated cytocoxicity (ADCC) and complement fixation. The CC binding domain polypeptide is capable of specifically binding to an experience of the polymucleotide encoding the construct comprising the polymucleotide encoding the construct comprising the polymucleotide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression construct, producing the binding domain-immunoglobulin fusion protein, a producing the binding domain-immunoglobulin fusion protein, a composition comprising the binding domain-immunoglobulin fusion protein, a polymucleotide and a carrier, and treating a subject carrier or polymucleotide and a carrier, and treating a subject thaving or suspected of having a malignant condition or a B-cell disorder. The binding domain-immunoglobulin fusion protein is useful for treating a condition or a B-cell disorder. The inding domain-immunoglobulin fusion protein is useful for treating a condition or a B-cell disorder. The inding domain condition or a B-cell disorder. The inding domain fusion protein sequence is a binding domain condition or a B-cell disorder. The inding domain fusion protein sequence is a binding domain condition or a B-cell disorder. The protein sequence is a binding domain condition or a B-cell condition fusion protein-associated protein sequence. Note: The condition of the printed specification at the sequence in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.
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493
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SLSLSPG 499
                                                          SLSLSPG
                                                                                                                                                               EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK
                                                                                                                                                                                                                                             TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDVWGTGTTVTVSSDQEPKSCDKTHTCPPSPAPELLGGPSVFLFPPKPKDTLMISRTPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---TANSDTHLLQ-GQSLTLTLESPPGSSPSVQCR-----SPR-----SPR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRSLWDQG-NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADS
                                                                                                                        EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID-----IVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAIYPGNGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GKNIQGGKTLSV-----SQLELQDSGTWTCTVLQNQKKVEFK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGGGGSSQAYLQQSGAELV-----RPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQSPAILSASPGEKVTMTCRASSSVS-YMHWYQQKP----GSSPKPWIYAPSNLASGVPA
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                                                          431
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Pred. No. 2.3e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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sinding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; CH3 constant region; IdG1:
                                                                                                                                                17-JAN-2001;
17-JAN-2002;
                                                                                                                                                                                                                                      25-JUL-2002; 2002US-00207655
                                                                                                                                                                                                                                                                                                    26-JUN-2003
                                                                                                                                                                                                                                                                                                                                                           US2003118592-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rheumatoid arthritis; myasthenia gravis; Grave's disease;
type I diabetes mellitus; multiple sclerosis; autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    malignant condition; B-cell disorder; melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Binding
                                                             (GENE-) GENECRAFT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain-immunoglobulin fusion protein-associated protein
                                                                                                                 2001US-0367358P.
2002US-00053530.
2002US-0385691P.
Hayden-Ledbetter MS,
   Thompson PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carcinoma; sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antithyroid;
eavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #114
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subject having or suspected of having a mali disorder, e.g. melanoma, Grave's disease or New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell autoimmune disease

WPI; 2003-801317/75.

Disclosure; SEQ ID NO 240; 157pp; English.

Comprising a binding domain-lemnunoglobulin fusion protein comprising a binding domain-lemnunoglobulin hings region polypeptide, an immunoglobulin heavy chain comprising region polypeptide, an immunoglobulin heavy chain complete that is fused to the hinge region polypeptide, and an immunoglobulin heavy chain complete that is fused to the hinge region polypeptide that is fused to the hinge region polypeptide. Comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin hinge region polypeptide (contains 2 cysteine residues, where the first cysteine is of mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the first cysteine is not mutated; a contains 2 cysteine residues where the first cysteine is not mutated; a contains 2 cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (c) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains con cysteine residues, where the mutated human IgG1 immunoglobulin hinge region cysteine residues, where the mutated human IgG1 immunoglobulin fluston protein is completed form (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin fluston protein is capable of at least one immunological activity comprising antibody capable of at least one immunological activity comprising antibody. The complete contains a cysteine residues in munoglobulin fluston protein is construct comprising the polymucleotide is capable of specifically binding to an antigen. Also included are an isolated polymucleotide encoding the binding domain polypeptide is capable of specifically binding to a promoter), a host cell transformed or transferted with a recombinant expression construct comprising the binding domain munoglobulin fluston protein, a construct comprising the binding domain and treating a subject having or suspected of having a malignant c

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ADD25679 RESULT

ADD25679 standard;

protein; 500

15-JAN-2004

(first entry)

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RESULT 98
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ID AARA
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XX AARA
XX AARA
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DT 25-D
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XX Hume
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Best Local S
Matches 274
  Carter
                                               14-JUN-1991;
                                                                         15-JUN-1992;
                                                                                               23-DEC-1992
                                                                                                                      W09222653-A1
                                                                                                                                                                      Humanisation;
                                                                                                                                                                                            H52H4-160 murine anti-CD18 antibody heavy chain
                                                                                                                                                                                                                    25-MAR-2003
12-MAY-1993
                                                                                                                                                                                                                                                                              AAR30774 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not identified the sequences in the printed specification by their SEQ ID number therefore none of the sequences can be explicitly identified.
                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hes 274;
                                                                                                                                              musculus
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                                                                                                                                                                                                                                                                                                                                            SLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY
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  Presta LG
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(first entry)
                                                                                                                                                                      rapid;
                                               91US-00715272
                                                                         92WO-US005126
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                                                                                                                                                                      monoclonal
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Pred. No. 2.3e-62;
27; Mismatches 94;
                                                                                                                                                                      antibody
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Best Local S
Matches 274
                                                                                                   Antibody; humanised; variable region; heavy chain; light chain; interferon gamma; IFN; treatment; prevention; septic shock; cachexia; immune disease; multiple sclerosis; Crohn's disease; skin disorders; inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv;
                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is that H52H4-160. (Updated c
 Domain
                     Peptide
                                                          Mus
                                                                    Synthetic
                                                                                          multivalent;
                                                                                                                                                              D9D10 heavy
                                                                                                                                                                                                                                   AAW85689
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                                                                                                                                                                                      12-AUG-1999
                                                          musculus
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                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                        SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                      VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
                                                                                                                                                                                                                                                                                                                                                                                                   KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LODSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC-
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                                                                                                                                                                                                                                                                                           SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                       VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
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1. .20
/note= "D9D10 light chain
21. .137
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                                   Location/Qualifiers
                                                                                                                                                                                                                                  protein;
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Pred. No. 2.2e-62;
4; Mismatches 88
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          peptide"
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New antibodies which bind and neutralise interferon-gamma (IFN gamma) can come used as a medicant, for preventing or treating septic shock, cachexia, commune diseases including multiple sclerosis and Crohn's disease and skin compared in the comparation of the disorders including bullous, inflammatory and neoplastic dermatoses. The cantibody is selected from a single chain antibody (scFV), a chimeric cantibody or diabody comprising the humanised variable domain of the cor a ruminant antibody. The antibody B9D10; a multivalent antibody; cor a ruminant antibody. The antibodies are also useful for determining cor a ruminant antibody. The antibodies are also useful for determining cor a ruminant antibody. The antibodies are also useful for determining cor a ruminant antibody. The antibodies are also useful for determining cor a ruminant antibody. The antibodies are also useful for determining cor a ruminant antibody. The antibodies are also useful for determining cor a ruminant antibody. The antibodies are also useful for determining cor a ruminant antibody. The antibodies are also useful for determining cor a ruminant antibody. The antibodies are also useful for determining cor a ruminant antibody. The antibodies are also useful for determining constant constant collaborate manual flag and a bample. Two fusion collaborate complement binding suther constant region. The heavy chain variable domain and a human comprised collaborate pour overlapping synthetic oligonucleotides (AAX08595) to generate pour overlapping synthetic oligonucleotides (AAX08590) to generate pour overlapping synthetic oligonucleotides (AAX08591) to amplified from poemic synthetic oligonucleotides (AAX08591) to applie to a two primers (AAX08591) and then cloned to repeat the complete 
                                                                                                                                                 Query Match
Best Local Similarity
Matches 277; Conserv
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18-JUN-1998;
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VILSQVQLVQSGSE-----LKKPGASVKISCKAS---GYTFTDYGMNWVKQAPGQG---L 65
                                                                        LLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLT
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                                                                                                                                             31;
                                                                                                                                             Score 1265.5; DB 2;
Pred. No. 2.3e-62;
Pred. Mismatches 79;
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KGPSKLNDRADSRRSLWD-QGNFP---

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18-AUG-1997;
18-JUN-1998;
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Peptide
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97EP-00870122.
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                                                                                                                                                                                   /note= "Human IgG1 heavy chain constant
                                                                                                                                                             note= "Leu added by cloning strategy"
                                                                                                                                                                                                             note= "Humanised heavy chain variable domain of D9D10"
                                                                                                                                                                                                                                   label Mouse_D9D10_light_chain_signal_peptide
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|73. .711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New engineered antibodies which bind and neutralise interferon-gamma - useful for prevention and treatment of septic shock, cachexia, immune diseases and skin disorders.
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N-PSDB; AAW85692.
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al Similarity 57.2%;
277; Conservative 3
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                                                                                                  LSPG 431
                                                                                                                                                    SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHWHYTQKSLS
                                                                                                                                                                                                   VSNKALPASIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
                                                                                                                                                                                                                      VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWE 367
                                                                                                                                                                                                                                                                                        VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ---KTLSVS-----TWTCTVLQNQKK 192
                                                                                                                                     SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
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1; Mismatches 79;
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X KIRDLINE=2238257; PubMed=12477932;

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X Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

X Altschul S.F. Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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X Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X Hopkins R.F., Jordan R.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

X Hopkins R.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

X Haha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

X Hohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Hilalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

X Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

X Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

X Hilalon D.K., Touchman J.W., Green E.D., Dickson M.C.,

X Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

X RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Homo sapiens (Human).
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Pr:
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01-OCT-2003 (TrEMBLrel. 2:
                                       TISSUE=Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W.,
Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/Genl
EMBL; BX538118; CAD98026.1; -.
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"Generation and initial analysis of more than 15,0 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                          Hypothetical protein DKFZP686N02209.
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  482 AA;
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il. 25, Last sequence update)
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RC TISSUE-Spleen;

RX MEDLINE-22388557 pubMed=12477932;

RM Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RISUE-Spleen;

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Joddin T.B., Toshiyuki S., Carninci P., Prange C.,

Ra Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Ra Ba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bossk S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Robert S., Korley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Haltschul S., Korlman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
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Matches
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Q7Z7P5;
Q1-OCT-2003
Q1-OCT-2003
Q1-OCT-2003
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
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Pred. No. 3.3e
29; Mismatches
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Last sequence update)
Last annotation update)
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Catarrhini; Hominidae;
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01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
FLJ00385 protein (Fragment).
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01-OCT-2002
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                                                                                                                                       Homo sapiens (Human).
Homo sapiens (Human).
'arvota; Metazoa; Chordata;
'arvota; Primates;
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Submitted (APR-2003) to the
EMBL; BC051328; AAH51328.1;
Hypothetical protein.
SEQUENCE 469 AA; 51395 MY
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"Generation and initial analysis
and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99;
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Pred. No. 8.16
                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Takano

no J., Kikuno R., Nagase sequence of a long cDNA

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Matches 262
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Q96PQ8,
01-DEC-2001 (TrEMBLrel. 19, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Factor VII active site mutant immunoconjugate.
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EMBL; AK090464; BAC03445.1; -.
PIR; A45874, A45874.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-cl.
InterPro; IPR003597; Ig-dl.
FinterPro; IPR003597; Ig-MHC.
Pfam; PF00047; 1g; 3.
SMART; SM00407; IGcl; 3.
                                                                                                 "Targeting tissue factor on tumor vascular endothelial cells a cells for immunotherapy in mouse models of prostatic cancer."; Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
Hu Z., Garen A.;
Submitted (FEB-2003) to
                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=21477448; PubMed=11593034;
Hu Z., Garen A.;
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                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPELQLEESCAEAQDGELDGLWTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPSREEMTKNOVSLTCLVKGFYPSDIAVEWESSGOPENNYNTTPPMLDSDGSFFLYSKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPSRDELTXNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REEQYNSTYRVYSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCP-APEPKSCDKTHTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNHKPSNTKVDKRVELK----TPLGDTTHTCPRCPEPKSCDTPP---PCPRCPEPK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REEQFNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HWTLPGPSWIDKNQGASAPWAQLCPTPQSHGAISLAASTKGPSVFPLAPCSRSTSGGTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             509 AA; 56111 MW; 089498D8076E863C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.3%;
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  the
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  EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1252;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; l
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                    Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .8e-94;
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1 01-OCT-2003 (TrEMBLrel. 27
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Matches 228
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GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:000559; F:calcium ion binding; IEA.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0006598; P:proteclysis and peptidolysis; IEJ.

R InterPro; IPR000152; Asx. hydroxyl_S.

R InterPro; IPR000152; Asx. hydroxyl_S.

R InterPro; IPR000181; EGF_Ca.

R InterPro; IPR001881; EGF_Ca.

R InterPro; IPR001881; EGF_II.

R InterPro; IPR001881; EGF_II.

R InterPro; IPR002383; GIA_blood.

R InterPro; IPR002383; GIA_blood.

R InterPro; IPR003597; Ig_Cl.

                                                                                                                                                                                                                                                                                                                                                  Interpro; IPRO01254; Peptidase_S1.
Interpro; IPRO01314; Peptidase_S1A.
Interpro; IPRO01294; VitK_dep_GLA.
Interpro; IPRO00294; VitK_dep_GLA.
Pfam; PF00008; EGF; 2.
Pfam; PF00008; EGF; 2.
Pfam; PF00047; ig; 2.
Pfam; PF00049; trypsin; 1.
PFINTS; PR00010; EGFBLOOD.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00011; EGF; 2.
SMART; SM00181; EGF; 2.
SMART; SM001069; GLA; 1.
SMART; SM001069; GLA; 1.
SMART; SM00020; Tryp_SPG; 1.
PROSITE; PS00101; ASX HYDROXYL; 1.
PROSITE; PS001186; EGF 2; 1.
PROSITE; PS001186; EGF 2; 1.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS001186; EGF CA; 1.
PROSITE; PS001187; EGF CA; 1.
PROSITE; PS001187; EGF CA; 1.
PROSITE; PS001187; IGLU CARBOXYLATION; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_SGR; 1.
PROSITE; PS00134; TRYPSIN_SGR; 1.
PROSITE; PS00135; TRYPSIN_SGR; 1.
                               375
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622
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                                                                                                                                                                                                                                                                                   228;
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                                                                                                                                         DPEVKFNWYYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
                                                                                                                                                            DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
                                                                                                                                                                                                              PFPGSAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
                                                                                                                                                                                                                                   PCP-APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                  NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                           APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
                                                                   APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                    44.9%;
96.2%;
                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                 Score 1213; DB 4; Length 679;
Pred. No. 4.3e-91;
l; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                          1,
0B0023AE70A067A1 CRC64;
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RESULT
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Q86TT2 PREMEATED.
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MC.
InterPro; IPR0030596; Ig_v.
Pfam; PP00047; Ig; 4.
SMART; SM00407; IGcl; 3.
SMART; SM00407; IGcl; 3.
SMART; SM00405; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_MHC; 2.
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Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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Submitted (JUN-2002) to the
EMBL; BC033178; AAH33178.1;
PIR; A60764; A60764.
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Similarity 51.5%;
61; Conservative 4
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Li W.B., Gruber C., Jessee J., Polayes D.;
"Full-length cDNA libraries and normalization.";
submitted (FEB-2003) to the EMBL/GenBank/DDBJ da
EMBL; BX248278; CAD62606.1; -
GO; GO:00468271; C.extrachromosomal DNA; IEA.
lnterPro; IPR007110; Ig-like.
lnterPro; IPR003597; Ig_cl.
lnterPro; IPR003597; Ig_cl.
lnterPro; IPR00306; Ig_MHC.
Hypothetical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chc
Mammalia; Eutheria; Pri
NCBI_TaxID=9606;
                                                        Q8TC63;
Q8TC63;
01-JUN-2002
01-JUN-2002
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50835; PROSITE; PS00290; Plasmid.
NON TER 1
SEQUENCE 354 AA;
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SMART; SM00407; IGc1; 3.
PROSITE; PS50835; IG_LIKE;
PROSITE; PS00290; IG_MHC;
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Submitted
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Primates;
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              Primates;
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Pred. No. 7.7e-87;
5; Mismatches 45;
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             Craniata; Vo
Catarrhini;
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                                                         sequence up
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                         Vertebrata; Euteleostomi;
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              Hominidae;
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Matches 262
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IG-V; 1.
PROSITE; PS00196; COPPER BLUE; 1
PROSITE; PS00196; COPPER BLUE; 1
PROSITE; PS0035; IG_LIKE; 4.
PROSITE; PS00390; IG_MHC; 3.
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SEQUENCE FROM N
TISSUE=Kidney;
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Equus caballus (Horse).
Eukaryota; Metazoa; Chordata;
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GO:0005499; F:electron transporter act
GO:0006118; P:electron transport; IEA.
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
in gamma 1 heavy chain constant region (
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   Vertebrata;
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RESULT 10
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Matches 179;
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InterPro; IPR003597; Ig c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF000407; Ig; 2.
SMART; SM00407; IGc1; 2.
SMOSITE; PS50835; IG_LIKE; 3.
PROSITE; PS50835; IG_MHC; 2.
NON TER
1 1 37 AA; 37438 MM;
                                                                                                                                                                                                                                                                                 Q7TMK1;
01-OCT-2003
01-OCT-2003
SEQUENCE FROM N.A.
STRALN=CZECH II; TISSUE=Breast tumor;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse I
Klausner R.D., Collins F.S., Wagner L.,
Altschul S.F., Zeeberg B., Buetow K.H.,
                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                           01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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Immunobiology 199:105-119(1998).
EMBL; AJ300675; CAC44624.1; -.
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NCBI_TaxID=9796;
[1]
                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                  Q7TMK1
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Leibold W., Radbruch A.;
"Organization of the equine immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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QALPQPIERTITKTKGRSQEPQVYVLAPHPDELSKSKVSVTCLVKDFYPPEINIEWQSNG
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larity 59.1%;
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Rodentia;
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Pred. No. 9.8e-67;
0; Mismatches 60
                                                                                                                                                                        Craniata; Vertebrata;
Sciurognathi; Muridae;
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c-gamma, c-epsilon and c-alpha go
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annotation update)
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L.H., Derge J.G.,
Shenmen C.M., Schuler
Schaefer C.F., Bhat N
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Matches 196
                                                                             01-MAY-2000
01-MAY-2000
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Q9R1A4;
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                                                    Gamma 1
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"Generation and initial analysis
and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:
  musculus (Mouse)
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                                            (Fragment).
                                                                             Created)
Last sequence up
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Pred. No. 3.2e-64;
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RESULT
Q8R3V9
ID Q8
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DT 1G

Q8R3V9 P Q8R3V9; Q1-JUN-2002 (Q1-JUN-2002 (Q1-OCT-2003 (Hypothetical IGH-4.

(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

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Last sequence update)
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Best Local S
Matches 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    wilde K.G., Yu.X., Ekramoddoullah A.K.M., Misra S.;

"Cloning of cDNAs encoding for anti-white pine blister rust

antibody (Mab 7, its light and heavy chains) and constructi

single chain antibody (scFV).";

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, #F152372; ADA40243.1; -.

R PIR; B45837; B45837.

R PIR; B45837; B45837.

PDB; 1CQK; 11-SEP-99.

R PDB; 1CQK; 11-SEP-92.

R PDB; 1CQK; 11-MAY-02.

R MGI; MGI:96446; IGh-4.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003066; Ig_MHC.

InterPro; IPR003066; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                              345
                                                                       340
                                                                                                                                                  228
                                                                                                                                                                                                  173
                                                                                                                                                                                                                                                   113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00047; ig; 3.
'; SM00406; IGv; 1.
TE; PS50835; IG_LIKE; 4.
TE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     188;
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SNWEAGNTFTCSVLHEGLHNHHTEKNLSHSPG
             SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                             RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
                                                                                               ---SSVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREE
                                                                                                                                                             LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                AAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQS
                                                                                                                                                                                                                                                                                                                           --- DOGNEPLIIKNIKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLE
                                                                                                                                                                                                                                                                                                                                                    LVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVASFSSGGIIYYTDSVKGRFTIY
                                                                                                                                                                                                                                                                                                                                                                           LGKKGDTVELTCTAS---QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLW
                                              KEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQK
                                                                                                                                                                                                                         ELO-----DSGTW----
                                                                                                                                                                                                                                                                         SPPGSSPSVQCRSP------SVSQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      48142 MW;
                                                                                                                                                                                                                                                                                                                                                                                                     66;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 867.5; DB 11;
Pred. No. 6.6e-63;
6; Mismatches 123;
                                                                                                                                                                                                                        -TCTVLQ--NOKKVEFKIDIVPCPAPEPKSCDKTHTCPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                      5C3A7BB3EE7D697C CRC64;
                       431
436
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Best Local S
Matches 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS508290; IG_MHC; 1.
                                                                                                                                                           Q99LC4;
Q99LC4;
01-JUN-2001
01-JUN-2001
01-OCT-2003
Similar to R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024405; AAH24405.1; -.
PIR; B45837; B45837.
MGD; MGI:96446; Igh-4.
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Mammalia; Eutheria;
NCBI_TaxID=10090;
                                          NCBI_TaxID=10090;
                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. seQUENCE 469 AA; 5
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    SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367
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192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 LGKKGDTVELTCTAS------QKKSIQFHWKNSNQIKILG--NQGSFLTKGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKTL-SVSQLELQ-----DSGTW-----TCTVLQ--NQKKVEFKIDIVPCPAPEPKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGQSLTLTLESPPGSSPSVQCRSP------RGKNIQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIS-RDNSQSILYLQMN-----ALRAEDSATYYC-ARDRRSSYYY-----SGTSFAY
                                                                                                                                                                                                                                                                                                                                                                                                  FVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG
                                                                                                                                                                                                                                                                                                                                                                                                                          FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                             1 (TrEMBLrel. 17, Creat
1 (TrEMBLrel. 17, Last
3 (TrEMBLrel. 25, Last
RIKEN cDNA 1810060009
                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.8%;
                                                                       Chordata;
Rodentia;
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Rodentia;
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Pred. No. 4e-6;
67; Mismatches
                                                                  Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                             sequence update) annotation updat gene.
                                                                                                                                                                                                                                                                               463
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                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                  468
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Best Local Similarity
Matches 191; Conserv
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MGD; MGI:96446; IGh-4.

InterPro; IPR007110; Ig_MHC.

InterPro; IPR003006; Ig_WC.

InterPro; IPR003596; Ig_V.

Pfam; PP00047; Ig; 3.

SMART; SM00406; IGV; 1.

PROSITE; PS00209; IG_MHC; 1.

PROSITE; PS00209; IG_MHC; 1.

SEQUENCE 463 AA; 51007 MW; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-2001) to the EMBL; BC003435; AAH03435.1; PIR; B45837; B45837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
413
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                                                                             NSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRD
 IMDTDGSYFIYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG
                                                                                                                                                                        -RGKNIQGGKTL-SVSQLELQ------DSGTW-----TCTVLQ--NQKKVEFKIDIVP
                                                                                                                                                                                                    YSYDLFAYWGQGTLVTVSAAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTW
                                                                                                                                                                                                                      ---DTHLLQGQSLTLTLESPPGSSPSVQCRSP------
                                                                                                                                                                                                                                             KATLTTDKSSSTAYMH------LSSLTSEDSAVYFC------ARSSY 120
                                                                                                                                                                                                                                                               PSKL-NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANS--
                                                                                                                                                                                                                                                                                   LARPGASVRLSCKASGYTFTGYGVSWVKQRTGQGLEWVG----EIYPGSGNTYYSEKFKG
                                                                                                                                                                                                                                                                                                       LGKKGDTVELTCTAS-----QKKSIQFHWKNSNQIKILGNQG----
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                   31.4%;
                                                                                                                                                                                                                                                                                                                          63;
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                                                                                                                                                                                                                                                                                                                          Score 848.5; DB 11; Length 463; Pred. No. 2.6e-61; Indels 105;
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                    431
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RESULT 14
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AC Q99L3
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DT 01-O
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OS Mus m
OC Eukas
OC Mamma
OC MAMMa
OC NCBI
RA SETAU
RA SETAU
RA SETAU
RA SUBAL;
DR Inter
DR Inter
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Q99L31;
01-JUN-2001 (TrEMBLrel. 17, Creat
01-JUN-2001 (TrEMBLrel. 17, Last
01-OCT-2003 (TrEMBLrel. 25, Last
Similar to RIXEN CDA 1810060009
                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                         Submitted (FEB-2001) to the EMBL; BC003878; AAH03878.1; PDB; 2AP2; 24-NOV-99. InterPro; IPR007110; Ig-like
                                                                                                                     NCBI_TaxID=10090;
                                                                                Strausberg R.;
                                                                                             SEQUENCE FROM N.A.
               InterPro;
  IPR003006;
: Ig-like.
: Ig_MHC.
: Ig_v.
                                                                  EMBL/GenBank/DDBJ
                                                                                                                                    Craniata; Vertebrata;
Sciurognathi; Muridae;
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(on update)
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                                                                     databases
                                                                                                                                       Euteleostomi; 
; Murinae; Mus
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Db
 RC STRAIN=C57BL/JJ; TISSUE=Pancreas;

RX MEDLINE=21085660; PubMed=11217851;

RA Arakawa T., Shihagawa A., Shibatta K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Gassterland T., Gissi C., King B., Kochiwa H.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L.,

RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
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Best Local S
Matches 198
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Q9D8L4;
Q1-JUN-2001 (TrEMBLrel. 17, L)
Q1-JUN-2001 (TrEMBLrel. 25, L)
Q1-OCT-2003 (TrEMBLrel. 25, L)
181006Q09Rik protein.
IGH-1 OR 181006Q09RIK.
                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 468 AA; 51661 MW;
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SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKC----PAPNILGGESVFIFPEKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTITVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Last sequence up
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Pred. No. 4.3e-61;
5; Mismatches 123;
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Sciurognathi; Muridae;
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; Murinae; Mus
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di M.,
Lee N.H.,
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                                                                                                                                                                                                                                                                                                                     Mus.
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RESULT
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Q99L25;
Q99L25;
Q99L25;
Q99L25;
Q99L25;
Q99L25;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence upda Q1-JUN-2003 (TrEMBLrel. 25, Last annotation up Similar to RIKEN CDNA 1810060009 gene.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Verteb Mammalla; Eutheria; Rodentia; Sciurognathi; Mu
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MGD; MGI:96443; Igh-1.
InterPro; IPR007010; Ig-like.
InterPro; IPR003106; Ig_WHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; ig; 3.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 473 AA; 51699 MW; 5
     Strausberg
Submitted (
                                                                                      NCBI_TaxID=10090;
                                                        SEQUENCE FROM N.A.
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EMBL; AK007918; BAB25349.1; -.
PIR; S26746; S26746.
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3 R.;
(FEB-2001)
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40.0%; Pred. No. 4.66
tive 67; Mismatches
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        the
     EMBL/GenBank/DDBJ databases
                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Matches 193
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HSSP; P01842; 7FAB.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_W-.
Pfam; PF00047; Ig; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_MHC; 1.
SEQUENCE 473 AA; 52449 MW; 1
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Q91Z05;
Q1Z05;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-OCT-2003 (TrEMBLrel. 2
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ dat EMBL; BC010327; AAH10327.1; -.

MGD; MGI:2144967; AU044919.

GO; GO:0005489; F:electron transporter activity;

GO; GO:0006118; P:electron transport; IEA.

InterPro; IPR000345; CytC heme BS.

InterPro; IPR000345; CytC heme BS.

InterPro; IPR000306; Ig_MHC.

InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                       Strausberg
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
AU044919.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSDAELVKPGASVKISCKVSGYTFTDHTIHW-----VKQRPEQGLEWIGYIYPRDGSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGNKVVLGKKGDTVELTCTASQKKSIQ--FHWKNSNQIKILGNQG-----SFLTKGPSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FVNNVEVLTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKALPAPIERTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P---PCKC----PAPNLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SVSQLELQ------DSGTW-----TCTVLQ--NQKKVEFKID-----IVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --WGQGTTITVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YNEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVCFCSRGGS-----IYYGYGLYYFDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNDRADSRRSLW---DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.5%;
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19,
25,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 823.5;
Pred. No. 3.1
                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE9889B7986DA155 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 3.

SMART; SM00406; IGv; 1.

PROSITE; PS00190; CYTOCHROME_C; PR051TE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.

Hypothetical protein—

SEQUENCE 473 AA; 51946 MW;
424
                       383
                                               364
                                                                       323
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            LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                              LDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPG
                                               KIKGLVRAPOVYILPPPARQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPV
                                                            KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPV
                                                                                               FVNNVEVHTAQTQTHREDYNSTIRVVSALPIQHQDWMSGKEFKCKVNNKDLPSPIERTIS
                                                                                                           YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                                                                                                       QSLTLTLESPPGSSPSVQ----CRSPRGKNI----
                                                                                                                                                                                                                                                                                                S-RDNAKNTLF-----LQMTSLRSEDTAMYYCARELWLRRID---
                                                                                                                                                                                                                                                                                                                        NDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQG
                                                                                                                                                                                                                                                                                                                                                 LVKPGGSRKLSCAASGFTFSDYGMHWVRQAPEKGLEWVAYINSGSTTIYYADTVKGRFTI
                                                                                                                                                                                                                                                                                                                                                                        LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILG----NQGSF-----LTKGPSKL
                                                                                                                                                                                                TFPALLOSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCP-
                                                                                                                                                                                                                                               QGTTTTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVH
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 51946 MW;
                                                                                                                                                                                                                                                                                                                                                                                                          30.0%;
                                                                                                                                                                                                                     SQLELQDSGTW-----TCTVLQ--NQKKVEFKID-----IVPCPA
                                                                                                                                                                                                                                                                                                                                                                                                  61;
                                                                                                                                                                                                                                                                                                                                                                                                Score 809.5; DB 11, Pred. No. 4.4e-58; 1; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>'</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF625F008932AF12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
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472
                        431
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                                                                                                                                                                                                                                                                                                 -----YWG
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RESULT 18
Q8R3H6
 GO; GO:0005489; F:electron transporter ac
GO; GO:0006118; P:electron transport; IE:
InterPro; IPR000345; CytC heme_BS.
InterPro; IPR007110; Ig-1Ike.
InterPro; IPR007106; Ig_MHC.
InterPro; IPR003506; Ig_v.
Pfam; PF00047; Ig; 3.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                  Q8R3H6;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                             Hypothetical
AU044919.
                                                                                                EMBL; BC025447; AAH25447.1; MGD; MGI:2144967; AU044919.
                                                                                                                       Strausberg R.;
Submitted (MAR
                                                                                                                                                                           Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                Q8R3H6
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                    Mus musculus (Mouse)
PS00190;
                                                                                                                       (MAR-2002) to the
                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                          protein.
CYTOCHROME_C;
                                                                                                                                                                                                                                    21,
                                                                                                                                                                                                                                   Created)
Last sequence up
Last annotation
                                                                                                                       EMBL/GenBank/DDBJ
                                                                                                                                                                            Craniata; Vertebrata; Euteleosto
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                 474
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                                                                                                                        databases
                                                                                                                                                                                          Euteleostomi;
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RESULT 19
009261
10 00926
AC 00926
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DT 01-JI
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1997
01-JUL-1997
01-OCT-2003
CD4 (Fragmen
Corbet S., Barre-Sinoussi F., Allan J.S.;

"Relation between phylogeny of African green monkey CD4
their respective simian immunodeficiency virus genes.";

J. Med. Primatol. 26:120-128(1997).
EMBL; AF001225; AAB60872.1; -.
HSSP; P01730; INIQ.
GO; GO:0016020 C:nembrane; IEA.
GO; GO:0016955; P:immune response; IEA.
InterPro; IPR000973; CD4_TCAg.
                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-98017879; PubMed-9379478;
MEDLINE-98017879; PubMed-9379478;
Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J.,
Fomsgaard Barra-Sinoussi F., Allan J.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             009261
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SEQUENCE 4
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=60711;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecus sabaeus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------QGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQK 115
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25,
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Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
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Best Local S
Matches 148
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Best Local S
Matches 148
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PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON TER 1 1 1
NON TER 397 397
SEQUENCE 397 AA; 43945 MW;
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01-JUL-1997
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SEQUENCE
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                                                                                                                                               PRINTS; PRO0692; CD4TCANTIGEN SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                          "Relation between phylogeny of African green monkey CD4 their respective simian immunodeficiency virus genes.", J. Med. Primatol. 26:120-128(1997).
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=98017879; PubMed=9379478;
Fomsggaard A., Muller-Trutwin M.C., I
Corbet S., Barre-Sinoussi F., Allan
                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, C
Mammalla, Eutheria, Primates, C
Cercopithecinae, Cercopithecus.
                                                                                                                                                                       Pfam; PF00047; ig; 2.
PRINTS; PR00692; CD4TCANTIGEN
                                                                                                                                                                                 InterPro, IPRO00973; CD4 TCAG.
InterPro, IPRO07110; Ig-Tike.
InterPro, IPR003596; Ig_v.
Pfam; PF00047; ia. 2
                                                                                                                                                                                                                               GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune respons
                                                                                                                                                                                                                                                     EMBL; AF001221; AAB60868.1; HSSP; P01730; 1WIQ.
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=60712;
                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecus tantalus.
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                                   VVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLW
 DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPP
                      VVLGKKGDTVELTCNASQNTTTQFHWKNSNQIKILGKQGSFLTKGSSKLRDRIDSRKSLW
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IPR003596; Ig_v.
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                                                                 28.4%;
ilarity 85.5%;
Conservative 10
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85.5%; Pred.
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Last sequence update)
Last annotation update)
                                                                            Score 767; DB 6;
Pred. No. 1.1e-54;
                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Cercopithecidae;
                                                                                                                 CF7F2F5D82335B0D CRC64;
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                                                                 Mismatches
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No. 1.1e-54;
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n J.S.
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                                                                                        Length 397
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RESULT 22
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Best Local S
Matches 148
                                            Q95NE9;
01-DEC-2001
01-DEC-2001
01-OCT-2003
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01-JUL-1997
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CD4 (Fragmen
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Pfam; PF00047; 19; 2.
PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98017879; PubMed=9379478;
Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., M. Corbet S., Barre-Sinoussi F., Allan J.S.;
"Relation between phylogeny of African green monkey CD4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 009263
Cercopithecus pygerythrus 
Eukaryota; Metazoa; Chordi
                                 CD4 (Fragment)
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Mammalia; Eutheria; Primates;
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GO; GO:0006955; P:immune response;
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007111; Ig-Tike.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             their respective simian immunodeficiency virus genes.";
J. Med. Primatol. 26:120-128(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecus tantalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                 GSSPSVKCRSPRGKNIQGGRTLSVPQLERQDSGTWTCTVSQDQNTVEFKIDIV
                                                                                                                                                             GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV
                                                                                                                                                                                                          DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPP
                                                                                                                                                                                                                                                        VVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSSPSVKCRSPRGKNIQGGRTLSVPQLERQDSGTWTCTVSQDQNTVEFKIDIV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV
                                                                                                                                                                                             DQGCFSMIIKNLKIEDSETYICEVENKKEEVELLVFGLTANSDTHLLQGQSLTLTLESPP
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                                                                                                                                                                                                                                         VVLGKKGDTVELTCNASQNTTTQFHWKNSNQIKILGKQGSFLTKGSSKLRDRIDSRKSLW
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397 AA;
                                          (TrEMBLrel. (TrEMBLrel. )
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                                                                                         PRELIMINARY;
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 Chordata;
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Last annotation update)
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                                                                                                                                                                                                                                                                                              Score 767; DB 6;
Pred. No. 1.1e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Cercopithecidae;
 Craniata; Vertebrata; Euteleostomi;
                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                  A3CD031535A51524 CRC64;
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Best Local S
Matches 148
                                                                        EMBL; AF001223; AAB60870.1; -.
HSSP; P01730; 1WIQ
GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; I
InterPro; IPR00973; CD4 TCA9.
InterPro; IPR009710; Ig-Tike.
InterPro; IPR007110; Ig-Tike.
Pfam; PF00047; 1g; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., Corbet S., Barre-Sinoussi F., Allan J.S., "Relation between phylogeny of African green monkey CD their respective simian immunodeficiency virus genes."

J. Med. Primatol. 26:120-128(1997).
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01-JUL-1997 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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"Relation between phylogeny of African green monkey CD4
their respective simian immunodeficiency virus genes.";
J. Med. Primatol. 26:120-128(1997).
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SMART; SM00406; IGV; 1
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MEDLINE=98017879; PubMed=9379478;
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Pred. No. 1.1e-54;
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Best Local Similarity
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NON_TER 1
NON_TER 397
SEQUENCE 397 AA;
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MEDLINE=98017879; PubMed=9379478;

MEDLINE=98017879; PubMed=9379478;

Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., M.

Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., M.

Corbet S., Barre-Sinoussi F., Allan J.S.;

"Relation between phylogeny of African green monkey CD4

their respective similan immunodeficiency virus genes.";

J. Med. Primatol. 26:120-128(1997).

EMBL; AF001224; ABB60871.1;

HSSP; P01730; INIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response;
InterPro; IPR000973; CD4 TCAG.
InterPro; IPR007110; Ig-Iike.
InterPro; IPR00710; Ig-V.
Pfam; PF00047; Ig; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1997
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSS0835; IG_LIKE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00692; CD41
SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cercopithecinae; Cercopithecus.
NCBI_TaxID=60711;
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                                                                                                                                                                                                                                                      Similarity
GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV
                                                                                                                                                             VVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLW
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                                                                  DQGNFPLIKKIKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPP
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                                          DQGCFSMIIKNLKIEDSETYICEVENKEEEVELLVFGLTANSDTHLLQGQSLTLTLESPP
                                                                                                                                     VVLGKKGDTVELTCNASQKTTTQFHWKNSNQIKILGKQGSFLTKGSSKLRDRIDSRKSLW
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397 AA;
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Pred. No. 2.3e-54;
                                                                                                                                                                                                                                                   Score 763;
Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
--- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
ONE V-LIKE AND 3 C2-LIKE DOMAINS.
EMBL; APF001226; AABC0873.1; --
EMBL; APF07309; AACC25124.1; --
EMBL; APF07309; 1WIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Nuclear gene trees and the phylogenetic relationships of the mangabeys (Primates: Papionini).";

Mol. Biol. Evol. 15:892-900(1998).

-i- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipoprotein; Palmitate; Repeat.
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DOMĀIN <1 370 EX
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PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGY; 1.
Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
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Corbet S., Barre-Sinoussi F., Allan J.S.;
"Relation between phylogeny of African green monkey CD4
Their respective simian immunodeficiency virus genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1997 (TrEMBLrel. 04, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecinae; Cercopithecus.
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                                                                                                                                                                      DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 80-165 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98320644; PubMed=9656488;
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CD4 (T-cell surface ant
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Best Local S
Matches 210
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0006955; P:immune response; IE

InterPro; IPR000973; CD4 TCAg.

InterPro; IPR003599; Ig.

InterPro; IPR003596; Ig-

InterPro; IPR003596; Ig-

Pfam; PF00047; ig; 2.
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MEDLINE=22174698; PubMed=12186836;
LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
"Blockade of HIV-1 Infection of New World Monkey Cells Occurs
Primarily at the Stage of Virus Entry.";
J. Exp. Med. 196:431-445 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG LIKE; 1. SEQUENCE 457 AA; 50899 MW;
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Eukaryota; Metazoa; Chordata; Craniata; Vej
Mammalia; Eutheria; Primates; Platyrrhini;
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01-OCT-2003 (TrEMBLrel.
Lymphocyte antigen CD4.
Saimiri sciureus (Commor
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01-MAR-2003
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                                                                                                                                             QVFGLTANPDTHLLQGQSLTLTLESPPGSSPSVECTSPRGKRIRGRKTLSVSQLGIPDSG
                                                                                                                                                                                                                                                                      ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                             TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFP-PKPKDTLMIS
                                                                                                                                                                                                                                            ILGVQNYFVTRGQSKLTDRIDSKRSSWDRGSFPLLIKDARIEDSETYICEVESKKEEVEL
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RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
                                             TWKCTVFQHLELV-FEINIVVLAFQQASS----TVYKKEGEQVEFSFPLAFAAETLTGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                  27.6%; Score 746; DB 6;
40.3%; Pred. No. 7.1e-53;
ive 56; Mismatches 149
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25,
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Last annotation update)
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Pred. No. 6e-54;
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ni; Cebidae; Cebinae; Saim
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Best Local S
Matches 210
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; I
InterPro; IPR000973; CD4_TCAg.
InterPro; IPR003599; Ig.
InterPro; IPR003199; Ig-like.
InterPro; IPR003596; Ig_v.
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SMART; SM00409; IG; 3.
SMART; SM004006; IG; 1.
PROSITE; PS50835; IG; 1.
SEQUENCE 457 AA; 50878 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22174698; PubMed=12186836;
LaBonte J.A., Babcock G.J., Patel T., Sodroski J.;
"Blockade of HIV-1 Infection of New World Monkey Coprimarily at the Stage of Virus Entry.";
J. Exp. Med. 196:431-445(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lymphocyte antigen CD4.
Callithrix jacchus (Common marmoset).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Platyrrhini, Callitrichidae, Callithrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                           TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISR
                                                                                                                                                                                                                                       ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLLIKNLKIEDSDTYICEVEDQKEEVQL
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TWKCTVSQHLELV-FKINIVVLAFQQASS----TVYKKEGEQVEFSFP---
                                                                                                                                                                                                                                                                                                                 MNGGIPFRHSLLVLQLALLIAVTHGKTVVLGKKGEMVELPCETSLKKKLQFHWKTSNQIK
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Pred. No. 8.6e-53;
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Matches 155
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PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
SMART; SM0499 MW;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
T-cell surface glycoprotein CD4.
Delphinapterus leucas (Beluga whale).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0016020; C:membrane; IEA.
GO; GO:0016025; P:immune response;
InterPro; IPR000973; CD4 TCAG.
InterPro; IPR007110; Ig-like.
InterPro; IPR00756; Ig_v.
Pfam; PF00047; 1g; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Romano T.A., Ridgway S.H., Felten D.L., Quaranta V.; "Molecular cloning and characterization of CD4 in an "the whale Delphinapterus leucas."; Immunogenetics 49:376-383(1999).
EMBL; AF071799; AAD23738.1; -.
HSSP; P01730, 1WIQ.
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Monodontidae, Delphinapterus.
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                                                                         QVFRLTASSDTRLLLGQSLTLTLEGPSGSNPSVQWKGPGNKRKNEAKSLSLPQVGLQDSG
                                                                                                        LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                          VEVLPTWSPPVQ---PMALIVLGGVAGLLVFTGLGIFLCVRCRHR
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Pred. No. 5.6e-41
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Best Local Similarity
Matches 121; Conserv
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P79355;
01-MAY-1997
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CD4 antigen precursor.
Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                           Signal.
SIGNAL
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Pfam; PF00047; ig; 3.
Pfam; PF000692; CD4TCANTIGEN.
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GO; GO:0006955; P:immune response;
InterPro; IPR000973; CD4 TCA9.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
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Norimine J., Miyazawa T., Kawaguchi Y., Tohya Y., Kai C.,
"A cDNA encoding feline CD4 has a unique repeat sequence
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 181
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               NIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV
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                                             ELLVFGLTAKVDPSGSGGSSSSSTSTSTSIYLLQGQSLTLTLESPSSSNPSVQWKGPGNK
SKSGVHSLSLSQLELQESGTCTCTVSQSQKTLVFNTNIL
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474 AA;
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52243 MW;
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55.3%; Pred. No. 2.50
tive 30; Mismatches
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Last annotation update)
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Best Local Sim:
Matches 103;
                                                                                                   055054
055054;
01-JUN-1998
01-JUN-1998
01-OCT-2003
T4 surface g
CD4.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; 1g; 2. PRINTS; PR00692; CD4TCANTIGEN. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG LIKE; 1. SEQUENCE 457 AA; 51368 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 84:7644-7648(1987).

EMBL, M17080; AAA37402.1; -

EMBL, M17076; AAA37402.1; JOINED.

EMBL, M17077; AAA37402.1; JOINED.

EMBL, M17079; AAA37402.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response;
InterPro; IPR000973; CD4 TCAG.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
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MEDLINE=88041159; PubMed=2823269;
Gorman S.D., Tourvieille B., Parn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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Mammalia; Eutheria;
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"Structure of the mouse gene encoding
                                                                                                   1-JUN-1998 (TrEMBLrel. (
1-JUN-1998 (TrEMBLrel. (
1-OCT-2003 (TrEMBLrel. 2
1-OCT-2003 (TrEMBLrel. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KILGNQG-SFLTKG--PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE
                                                                                                                                                                                                                                                                                                                                                      VQDSDFWNCTVTLDQKK 196
                                                                                                                                                                                                                                                                                                                                                                                                    LODSGTWTCTVLQNOKK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVELWVFKVTFSPGTSLLQGQSLTLTLDSNSKVSNPLTECKHKKGKVVSGSKVLSMSNLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVQLLVFGLTANSDTHLLQGQSLTLTLES-PPGSSPSVQCRSPRGKNIQGGKTLSVSQLE
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                                                                                                                                                                                                                                 PRELIMINARY;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.3%; Score 467; DB 11; 52.3%; Pred. No. 6.7e-30; tive 32; Mismatches 56;
                                                                                                      06, Created)
06, Last sec
25, Last and
(Fragment).
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01, Last sequence update)
25, Last annotation update)
                                                                                                                             Last sequence up
                                                                                                                                                                             Created)
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encoding CD4
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       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local Similarity
Matches 92; Conserv
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O77596;
O17696;
O1-NOV-1998 (TrEMBLrel. 08, La
01-NOV-1998 (TrEMBLrel. 25, La
T-cell surface glycoprotein Cl
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NON TER
SEQUENCE
                                                                                           MEDLINE-98320644; PubMed=9656488;
Harris E.E., Disotell T.R.;
"Nuclear gene trees and the phylogenetic relationships of the mangabeys (primates: Papionini).";
Mol. Biol. Evol. 15:892-900(1998).
-!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maddon P.J., Molineaux S.M.,
Alt F.W., Chess L., Axel R.;
Submitted (FEB-1998) to the I
EMBL; AF045882; AAC01764.1;
HSSP; P01730; 1WBR.
                                                                                                                                                                                                                                                                                                                       (Fragment).

Mandrillus sphinx (Mandrill) (Papio sphinx).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

Cercopithecinae; Mandrillus.

NCBI_TaxID=9561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=88097446; PubMed=3501122; Maddon P.J., Molineaux S.M., Maddon D.E., Zimmerm Alt F.W., Chess L., Axel R.; Proc. Natl. Acad. Sci. U.S.A. 84:9155-9159(1987).
  +++
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                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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GO; GO:0006955; P:immune response;
InterPro; IPR000973; CD4 TCA9.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
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SIMILARITY).
SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
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433 AA;
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; 48590 MW; AB19330750A8499A CRC64;
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Last annotation updat
CD4 (T-cell surface a
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surface antigen
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Best Local S
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Matches 76
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mandrillus leucophaeus (Drill) (Papio leucophaeus). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Cercopithe Cercopithecinae; Mandrillus. NCBI_TaxID=9568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0016021; C:integral to membrane; InterPro; IPR007110; Ig-like. Immunoglobulin domain; T-cell; MHC; Tran NON TER 1 1 1 IG-LIKE V-TDOMĀIN <1 19 IG-LIKE V-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
HSSP;
GO; GC
                                                                                                                                                                                                                                                                                 -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
ONE V-LIKE AND 1 C2-LIKE DOMAIN.
EMBL; AF057387; AAC25131.1; -.
HSSP; P01730; 1CDY.
GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPR007110; Ig-like.
Inmunoglobulin domain; T-cell; MHC; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=98320644; PubMed=9656488;
Harris E.E., Disotell T.R.;
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P01730; 1CDY.
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76; Conserv
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KTLSVSQLELQDSGTWTCTVLQNQK 191
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nilarity 89.4%;
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Last annotation update)
CD4 (T-cell surface antigen
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                                                                              Score 400; DB 6; 1
Pred. No. 2.1e-25;
6; Mismatches 3;
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Pred. No. 2.1e-25;
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Best Local Similarity
Matches 76; Conserv
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O77599;
O1707599;
O1-NOV-1998 (TrEMBLrel. 08, Li
O1-NOV-1998 (TrEMBLrel. 25, Li
T-cell surface glycoprotein Cl
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NON TER 1
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DOMAIN 20
DISULFID 49
NON TER 86
SEQŪENCE 86 AF
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01-NOV-1998
01-NOV-1998
01-OCT-2003
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MOI. Biol. Evol. 15:892-900(1998).
-i- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
Cercopithecinae;
NCBI_TaxID=9565;
                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                       (Fragment).
Theropithecus gelada (Gelada baboon)
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GO; GC
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                                                              Eukaryota;
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Harris E.E., Disotell T.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=36225;
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                                                                                                                                                                                                                                                                                                                                                61 RILSVPQLERODSGTWTCTVSQDQK
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IPR007110; Ig-like.
bulin domain; T-cell; MHC; Transmembrane.
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                      Theropithecus.
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Primates;
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Last annotation update)
CD4 (T-cell surface antigen
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Pred. No. 3.7e-
5; Mismatches
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Last annotation update)
CD4 (T-cell surface antigen
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                                                                Craniata; Vertebrata; Euteleostomi
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RESULT 36
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Best Local S
Matches 75
                                      Query Match
Best Local Similarity
Matches 135; Conserv
                                                                                                                          Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ date EMBL; BC011857; AAH11857.1; -.

PIR; S15590; S15590.
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig_wHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS050835; IG_LIKE; 5.
PROSITE; PS05093; IG_MHC; 3.
PROSITE; PS05090; IG_MHC; 3.
PROSITE; PS05090; IG_MHC; 3.
SMOUNCE 613 AA; 67273 MW; 31214203FB8421E7 (2001)
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01-OCT-2003 (TrEMBLrel.
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SEQUENCE FROM N.A.
MEDLINE=98320644; PubMed=9656488;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>မ</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                  CISSUE=B-cel
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
ONE V-LIKE AND 1 C2-LIKE DOWAIN.
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RHLLLVLQLALLP-----AATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI
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                                           Conservative
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                                                               Score 395.5; DB 4;
Pred. No. 7.9e-24;
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Pred. No. 3.7e-25;
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O77595;
O1-NOV-1998 (TrEMBLrel. 08, C:
01-NOV-1998 (TrEMBLrel. 28, L:
01-OCT-2003 (TrEMBLrel. 25, L:
T-cell surface glycoprotein C)
                                                                                                                                                                                                                                                Cercocebus galeritus chrysogaster.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercocebus.
-!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
ONE V-LIKE AND 1 C2-LIKE DOMAIN.
EMBL; AF057382; AAC25126.1; -.
                                                                                           Harris E.E., Disotell T.R.,
"Nuclear gene trees and the phylogenetic relationships of the
"Nuclear gene trees and the phylogenetic relationships of the
mangabeys (primates: Papionini).";
Mol. Biol. 15:892-900(1998).
-i- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                        MEDLINE=98320644; PubMed=9656488; Harris E.E., Disotell T.R.;
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  NCBI_TaxID=75569;
                                                                                                                                                                                                                                                                                                                (Fragment).
                                                                              SIMILARITY)
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(T-cell surface antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAIN ONE V-LIKE AND 1 C2-LIKE DOMAIN.
EMBL; AP057388; AAC25132.1; -.
HSSP; P01730; 1CDY.
HSSP; P01730; 1CDY.
GO; GO:0016021; C:integral to membrane; IEA.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Glycoprotein; T-cell; MHC; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE-98320644; PubMed=9656488;

Harris E.E., Disotell T.R.;

Harris E.E., Disotell T.R.;

"Nuclear gene trees and the phylogenetic relationships of the "Nuclear gene trees and the phylogenetic relationships of the mangabeys (primates: Paplonini).";

Mol. Biol. Evol. 15:892-900(1998).

-i- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Papio sp. (Baboon).

Bukaryota; Metazoa; Chordata;

Mammalla; Butheria; Primates;

Cercopithecinae; Papio.

NCBI_TaxID=61183;
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01-NOV-1998 (TrEMBLrel 08, Last sequence update)
01-OCT-2003 (TrEMBLrel 25, Last annotation update)
T-cell surface glycoprotein CD4 (T-cell surface antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107
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                                                                                                                            l Similarity
74; Conserv
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llarity 87.1%;
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                                                                                                                         Score 392; DB 6;
Pred. No. 9.5e-25;
7; Mismatches 4
                                                                                                                                                                                                                                                                                                             IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
N-LINKED (GLCNAC. . .)
BY SIMILARITY.
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IG-LIKE C2-TYPE DOMAIN.
N-LINKED (GLCNAC. . .) (POTENTIAL)
BY SIMILARITY.
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Catarrhini; Cercopithecidae;
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Best Local S
Matches 116
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Q8WUK1;
01-MAR-2002
01-MAR-2002
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG LIKE; PROSITE; PS00290; IG MHC; 3 Hypothetical protein. SEQUENCE 613 AA; 67296 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (DEC-2001) to the EMBL; BC020240; AAH20240.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 5. SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; PL0120; PL0120.
PIR; S15590; S15590.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Tonsil,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro; IPR007110;
                      530
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448 GLWTT
                                                                                                                                                                                                                                                                                                                                                                                            116;
                                                                                                                                                                                                                                                                                                                        94 LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL-----QGQSLTLT
                                                                                                                                                                                                                                                                                                                                                                      36 TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                      RYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS----TEGEVSADEEGFE
                                     SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELD
                                                                 VYLLPPAREQLNLRESATITCLVTGFSPADVFVQMMQRGQPLSPEKYVTSAPMPEPQAPG
                                                                                VYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDG
                                                                                                              -----VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTH
                                                                                                                                                                                 HTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                        EAKESGPTTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR-
                                                                                                                                                                                                                              ELQDSG-------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT
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(TrEMBLrel.
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452
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                           Score 389.5; | Pred. No. 2.5e
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                        60C7F5950671E315 CRC64;
                                                                                                                                                                                                                                                                           ----SPR-----GKNIQGGKTLSVSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85
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                                                                                                                                                                                                                                                                                                                                                                                           ); DB 4;
1.5e-23;
1es 167;
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; Homo.
                                                                                                                                                                                                                                                                                                                                                                                           125;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  Matches 116;
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; BC009851; AAH09851.1; -.

PIR; S15590; S15590.

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:000355; P:regulation of transcription, DNA-dependent;
InterPro; IPR000005; HTHARAC.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   096GA6, PRELIMINARY; PRT; 614 AA.
096GA6, 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 5.

SMART; SM00406; IGv; 1 IGv; 1

PROSITE; PS00041; HTH ARAC FAMILY 1; PROSITE; PS0835; IG LIKE; 5.

PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical SEQUENCE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=B-cell;
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                                                                                                                                                                                                                                                                                                                                                         36 TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                                                                                                 ELQDSG-----
                                                                                                                                                                                                                                                              LESPPGSSPSVQCR------SPR-----GKNIQGGKTLSVSQL
                                                                                                                                                                                                                                                                                    SVLRGGKYAATSQVLLPSKD------VMQGTDEHVVCKVQHPNGNKEKNVPLPVI
                                                                                                                                                                                                                                                                                                                                    SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG-----FP
  RYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS-----TEGEVSADEEGFE
                                                                                             TNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPD
                                                                                                                                                                                                                                                                                                          LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL------QGQSLTLT
                       SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELD
                                              VYLLPPAREQUIRESATITCLVTGFSPADVFVQMMQRGQPLSPEKYVTSAPMPEPQAPG
                                                                       VYTLPPSRDELT-KNOVSLTCLVKGFYPSDIAVEWESNGOP--ENNYKTTPPVLD--SDG
                                                                                                          TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQ
                                                                                                                                                                  HTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                         EAKESGPTTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR-
                                                                                                                                                                                                                                       AELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQA
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614 AA; (
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                                                                                                                                          -VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTH
                                                                                                                                                                                                                                                                                                                                                                                                                               67921 MW; 55EF536E77AA9BBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                               14.4%; Sc
23.9%; Pr
tive 77;
                                                                                                                                                                                                              -----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT
                                                                                                                                                                                                                                                                                                                                                                               Score 389.5; DB 4; Length 614; Pred. No. 2.5e-23; Indels 125;
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Best Local Similarity
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5
PROSITE; PS00290; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 618 AA; 67758 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (NOV-2001) to the
EMBL; BC017356; AAH17356.1;
PIR; S15590; S15590.
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Lymph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
448 GLWTT 452
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                                                                                                                                                                                                                                                                                                                                                                                                                             14.4%;
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Q96AA6, PRELIMINARY; PRT; 618 AA.
Q96AA6; O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
535 RYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKS-----TEGEVSADEEGFE
                                                                                                                                                                                                                                                                                                                                                                214 HTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL------QGQSLTLT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LESPPGSSPSVQCR------SPR-----GKNIQGGKTLSVSQL
                                                                                                                                VYTLPBSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDG
                                                                                                                                                                                                          TNISESHPNATTSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPD
                                                                                                                                                                                                                                                                                                               -----VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVLRGGKYAATSOVLLPSKD------VMQGTDEHVVCKVQHPNGNKEKNVPLPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVAVGCLAODFLPDSITFSWKYKNNSDISSTRG------
                                              SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELD
                                                                                                                                                                                                                                                           TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELQDSG------TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQA
                                                                                                     VYLLPPAREQUNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 389.5; DB 4;
Pred. No. 2.5e-23;
77; Mismatches 167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96DBD4C7C696E0A6 CRC64,
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Best Local S
Matches 74
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Lophocebus albigena albigena.
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Primates; C
Cercopithecinae; Lophocebus.
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DOMĀIN 1
DOMAIN 20
DISULFID 49
NON TER 86
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-I SUBCULTES WITH P56-LCK (BY SIMILARITY).

-I SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).

-I SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE V-LIKE AND 1 C2-LIKE DOMAIN.

EMBL, AF057391, AAC25135.1; -

HSSP; P01730; ICDY.

HSSP; P01730; ICDY.

InterPro; IPR007110; Ig-like.
Strausberg K.;
Strausberg K.;
                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98320644, PubMed-9656488;
Harrie E.E., Disotell T.R.;
"Nuclear gene trees and the phylogenetic relationships of the mangabeys (primates: Papionini).";
mol. Biol. Evol. 15:892-900(1998).
-I-FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, 01-OCT-2003 (TrEMBLrel. 25, T-cell surface glycoprotein
                                                                                                                                                 Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                          TISSUE=Lymph;
                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTLSVPQLERODSGTWTCTVSQDQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YICEVEDKKEEVELLVFGLTANSDTHLLEGQSLTLTLESPPGTSPSVKCRSPRGKNIQVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR007110; IG-like.
bulin domain; T-cell; MHC; Transmembrane
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E
                the EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation updat
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Pred. No. 2e-24;
7; Mismatches
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Last annotation update)
CD4 (T-cell surface antigen
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                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RESULT
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Best Local
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Q9BQB8;
01-JUN-2001
01-JUN-2001
01-OCT-2003
                             Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006180; AAH06180.1; -.
EMBL; BC001872; AAH01872.1; -.
HSSP; P01825; 7FAB.
Interpro; IPR007110; Ig-like.
                                                                                                                                            Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
PROSITE; PS00290; IG MHC; 3
                                                                                                SEQUENCE FROM N. TISSUE=Muscle, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein. SEQUENCE 597 AA; 65274 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003006;
InterPro; IPR003596;
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HSSP; P01825; 71
                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
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                                                                                                                                                                                                                                                                                                                   LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                     ----VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNGNKEKNV----PLPVIAELPPKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG
                                                                                                                                                                                                                                                                                            LTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTG
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                                                                                                and Lymph;
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                                                                                                                                             Chordata;
Primates;
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Last sequence update)
Last annotation update)
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Pred. No. 5
                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                     PRT;
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.6e-23;
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InterPro; IPRO Pfam; PF00047; InterPro;

; IPR007110; Ig-like.; IPR003006; Ig_MHC.; IPR003596; Ig_v.
00047; ig; 5.

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RESULT
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Best Local S
Matches 114
Query Match
Best Local
                               Pfam; PF00047; ig; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS00290; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW;
                                                                                                                                                                                                                                                         Q96BB9;
01-DEC-2001
01-DEC-2001
01-OCT-2003
                                                                                         Strausberg R.;
Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_w.
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PROSITE; PS00290; IG_MHC; 3.
Hypothetical protein.
SEQUENCE 597 AA; 65300 MW;
                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                    Hypothetical protein. Homo sapiens (Human).
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                                                                                                                                                                     TISSUE=B-ce
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                 NCBI_TaxID=9606;
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Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNGNKEKNV----PLPVIAELPPKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG-----
                                                                                                                                                                                                                                                                                                                                                                                  LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                           RDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLYSK 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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Primates;
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                                 65039 MW;
14.2%;
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19,
25,
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Last annotation updat
                                                                                                                                                                                                                                                                                Created)
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Pred. No. 5
Score
Pred.
                                                                                                                                                                                                               Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                      PRT;
                                 4FCA3AD8ECE263D9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2DAFAD50A6375851 CRC64;
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385;
No. 5.
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                                                                                                                                                                                                                                                                                                       597
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5.6e-23;
 DB 4;
.6e-23;
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                                                                                                                                                                                                                Hominidae;
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          Length
                                  CRC64;
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RESULT 46
077600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            077600;
077600;
01-NOV-1998
01-NOV-1998
                                                                                               -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAIN
ONE V-LIKE AND 1 C2-LIKE DOMAIN.
EMBL; AF057390; AAC25134.1; -.
HSSP; P01730; 1CDY.
GO; GO:0016021; C:integral to membrane.
DOMAIN
CARBOHYD
DISULFID
                                         Immunogl
NON TER
DOMAIN
                                                                                                                                                                                                                                                                                                                                                         (Fragment).
Lophocebus aterrimus.
Lophocebus aterrimus.
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
Cercopithecinae; Lophocebus.
                                                                                                                                                                                                                Harris E.E., Disotell T.R.; "Nuclear gene trees and the phylogenetic relationships of the "Nuclear gene trees and the phylogenetic relationships of the mangabeys (primates: Papionini)."; Mol. Biol. Evol. 15:892-900(1998).

MOI. Biol. Evol. 15:892-900(1998).

-i- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-OCT-2003 (TrEMBLrel. 25, T-cell surface glycoprotein
                                                                                                                                                                                                                                                                                                    MEDLINE=98320644; PubMed=9656488;
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=75566;
                                                                                      nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36
                                                                      lobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLYSK 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTNISESH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIIKNLKIEDSDTYICEVED----QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAKESGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPSVQCR-----SPR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNGNKEKNV----PLPVIAELPPKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSI
                                                                   IPR007110; Ig-like.
bulin domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTG
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Last annotation update)
CD4 (T-cell surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN.
N-LINKED (GLCNAC. . .)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Catarrhini; Cercopith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                      T-cell; MHC;
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Cercopithecidae;
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                                                                         Transmembrane
                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                  T4/LEU-3)
                                                                                                                                                           CONTAINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            RC STRAIN-C57BL/6NCr; TISSUE-Hematopoietic Stem Cell;

RX MEDLINE-22388557; PubMedel12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschwid S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

RA Altscheho L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Altschards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Altschards S., Worley K.C., Hale S., Garcia
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Best Local &
Matches 73
                                                                                                                                                                                             Query Match
Best Local (
                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                           Hypothetical protein. SEQUENCE 614 AA; 6
                                                                                                                                                                                                                                                                                                   Submitted (JUN-2003) to the EMBL; BC053409; AAH53409.1;
                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C57BL/6NCr; TISSUE=Hematopoletic Stem Cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                               mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 YICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGG
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                                                                                                                                                                                             Similarity
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                                          SKLN-DRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTH 132
                                                                                                                              LGKKGDTVELTCTASQKKSIQFHWKN-----SNQIKILGN------QGSFLTKGP
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                                                                                      LVKPGASVKISCKAS-GYAFSSSWMNWVKQRPGKGLEWIGRVYPGDGDTNYNGKF--KGK
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3 (TrEMBLrel. 25,
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ilarity 23.3%;
Conservative 7
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                                                                                                                                                                                                                                                           67746 MW; 839BAF3B8D124F89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A. 99:16899-16903(2002).
                                                                                                                                                                      77;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 383; DB 6; I
Pred. No. 5.3e-24;
7; Mismatches 5;
                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases.
                                                                                                                                                                    Score 381; DB 11;
Pred. No. 1.2e-22;
77; Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A9D97A88464FE9BE CRC64;
    --LSSLTSEDSAVYFC-ARDYGSSYRFAYWG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 614
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                                                                                                                                                                                                            Length 614;
                                                                                                                                                                         Indels 210;
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맑
202 SVLKGGKYAATSQVLLESKUVMQGTUEHVVCKVQHENGNKEKNV----ELEVIAELEEKV
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94 LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS 149 :::	8 8
36 TVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP 93	ਲ ਝ
Query Match 14.1%; Score 380; DB 4; Length 588; Best Local Similarity 24.8%; Pred. No. 1.4e-22; Matches 113; Conservative 73; Mismatches 163; Indels 106; Gaps 15;	3 20
SEQUENCE 588 AA; 64438 MW; FC60DBAD82B39FD7 CRC64;	ő
300290; IG_MHC;	₹ ₩
IGV; 1. ; IG LIKE;	××
Pfam; PF00047; 19; 5.	₩;
2006;	¥ ¥
BC019235, AAH19235.1; ro; IPR007110; Iq-like.	××
Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.	£ £
SEQUENCE FROM N.A. TISSUE=Lymph;	ิ ซิ
NCBI_TaxID=9606;	2 ×
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	۲ ۲
Mothers Charles Cultiple Voitobusts directors	1 X 5
(TrEMBLrel. 25, Last annotation protein.	Ħ Ħ
20, Created) 20, Last sequence up	ä ä
PREDIMINARI; PAI	ລ໌
48	ESULT DBWUX4
539 TVTEEBWNSGETYTCVVSHEALPHLVTERTVDXSTEGEVNAEEEGFENLWTT 590	퓻
396 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT 452	¥
479 EQLNLRESATVTCLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPEPGAPGFYFTHSIL 538	ğ
341 DELT-KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 395	¥
423 SAKGVASVCVEDWNNRKEFVCTVTHRDLPSPQKKFISKPNEVHKHPPAVYLLPPAR 478	퓻
286 RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 340	₹
365 FTIPPSFAD-IFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPNGTF 422	퓻
226 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 285	₹
305 TIENKGSTPQTYKVISTLTISEIDWLNLNVYTCRVDHRGLTFLKNVSSTCAASPSTDILT 364	퓻
221	₹
245 VAEMNPNVNVFVPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPV 304	퓻
KTHTCP	₹
188 VIQGIRTFPTLRTGGKYLATSQVLLSPKSILEGSDEYLVCKIHYGGKNKDLHVPIPA 244	ğ
164QGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPA 204	¥
130QGTLVTVSAESQSFPNVFPLVSCESPLSDKNLVAMGCLARDFLPSTISFTWNYQNNAE 187	ŏ
TLTLESPPGSSPSVQCRSP-RGKN	₹

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Best Local S
Matches 121
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Q8VCX7;
01-MAR-2002 (TrEMBLrel.:
01-MAR-2002 (TrEMBLrel.:
01-OCT-2003 (TrEMBLrel.:
                                                                                                                                                                                                                                                                                                                                   EMBL, BC018315; AAH18315.1; -
MGD; MGI:96448; Igh-6.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; /
                                                                                                                                                                                                                                                                                  Pfam; PF00047; 19; 5.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_KIKE; 5.

PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
                                                                                                                                                                                                                                                           Hypothetical protein. SEQUENCE 613 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                               rissue=Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                              206
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                                                                                                                                                                                                                    Similarity
                                         VPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPVTIENKGSTPQT
                                                                                                                        ---PLIIKNLKIEDSDTY-ICEVEDQKEEVQLLVFGLTANSDTHL----LQGQSLTLTLE
----KTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG
                                                                                             TSQVLLSPKSILEGSDEYLVCKIH-----YG-GKNRDLHVPIPAVAEMNPNVNVF
                                                                                                                                               VAMGCLARDFLPSTISFTWNYQNNTEVIQGIRTFPT-----LRTGGKYLA
                                                                                                                                                                          VELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNF--
                                                                  SPP-----GSSP----SVQCR----SPR-----GKNIQGG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPA
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                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
                                                                                                                                                                                                    13.8%; Score 373.5; DB 1
25.2%; Pred. No. 5.1e-22;
ative 87; Mismatches 157
                                                                                                                                                                                                                                                         67855 MW;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                           41A9384DD4C22862 CRC64;
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RESULT 50
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                                                                                                                                                                                                                        Query Match
Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Neuroblastoma;
Li W.B., Gruber C., Jessee J., Polayes D.;
"Full-length cDNA libraries and normalization.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ dat
EMBL; BX161420; CAD61894.1; -.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-cl.
InterPro; IPR003597; Ig-cl.
InterPro; IPR00306; Ig-MHC.
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Q86TT1;
Q86TT1;
Q86TT1;
O1-JUN-2003 (TrEMBLrel. 24, Cr.
O1-JUN-2003 (TrEMBLrel. 24, La.
O1-OCT-2003 (TrEMBLrel. 25, La.
Human full-length cDNA clone C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope;
Submitted
                                                                                                                                                                                                                                                                                              Pfam; PF00047; 19; 3.

SMART; SM00407; IGC1; 3.

PROSITE; PS50835; IG_LKE;

PROSITE; PS50290; IG_MHC; 3.

Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens (Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Neuroblastoma;
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                275
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                                                                                                                                   171 VSQLELQDSG-----TWTCTVLQ----NQKKVEFKIDIVPCPAPEPKSCDKTHTCPELL
                                                                                                                                                                25
                                                                                                                                                                                                                         l Similarity
98; Conserv
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQV
                                            CGPDQDTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGEAVKTHT
                                                                         GGPS-----VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
                                                                                                      QVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASS------M
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                                                                                                                                                                LPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTD
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                                                                                                                                                                                                                                                                                   375 AA;
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                   41272 MW;
                                                                                                                                                                                                                        13.6%; Score 366.5; DB 4; 28.6%; Pred. No. 9.6e-22; tive 59; Mismatches 125;
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e CSODD006YL02 of neuroblastoma
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                   7ACD1AF4399C5EFE CRC64;
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Best Local S
Matches 70
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01-OCT-2003
CD4 protein
                                                                                           Q7TOR1; PRELIMINARY;
Q7TOR1; 17EMBLrel 25,
01-OCT-2003 (TEMBLrel 25,
01-OCT-2003 (TEMBLrel 25,
01-OCT-2003 (TEMBLrel 25,
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NON TER
SEQUENCE
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Q13969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor gene].";

Vopr. Virusol. 40:100-102(1995).

EMBL; X87579; CAA60883.1; -.

EMBL; S79267; AAB35273.1; -.

EMBL; S79267; BAB35273.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zverev V.V., Blinov V.M., Nedospasov S.A.; "Splice-mediated insertion of antisence and sence Alu repeats "Splice-mediated insertion of three exons of CD4 mRNA."; CD4 gene: identification of three exons of CD4 mRNA."; Submitted (APR-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Zverev V.V., Blinov V.M.,
Hypothetical protein.

Renopus laevis (African clawed frog).

Renopus laevis (African clawed frog).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95407135, PubMed=7676667;
Zverev V.V., Sidorov A.V., Nedospasov S.A., Maliushova V.V.,
Udalova I.A., Andzhaparizde O.G., Blinov V.M.;
"[Nucleotide sequence of two exons of the human T-lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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GO:0004872; F:receptor activity; IEA.
erPro, IPR007110; Ig-11ke.
pcsn835; IG_LIKE; 1.
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Klausner R.D., Collins F.S., Wagner L., Schammen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan R., Toshiyuki S., Carninci P., Prange C.,

A Stapleton M., Soares M.B., Bondiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S. T. Marya M. A.,

A Jones S. T. Marya M. A.,

Jones S. T. Marya M. A.,

Jones S. T. Marya M. A.,

Jones S. T. Marya M. A.,

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Jones S. Jordan M. J. Jones J. J
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Klein S., Strausberg R.;
Submitted (AUG-2003) to the
EMBL; BC056078; AAH56078.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical SEQUENCE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Richardson
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NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKKGDTVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSF----LTKGPSKLNDRADSRR
  LVKGFYPSDIAVEW--ESNGQPENNYKTTP----
                                              CADEWNNDK-FVCKVEHTELASMKEVFLFKEKGEYNTPSVYVFPPPLEELSKRETATLTC
                                                                                  LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTC
                                                                                                                                 FEKKSATLTCLVSNMANSEDLRSISWFKKSGTQEIPLKTELGDAIYNDNRTYSVKGTTTV
                                                                                                                                                                            MISRTPEVTCVVVDVSHEDPEVKFNWY-VDGVEVHNAKTKPREEQYNS--TYRVVSVLTV
                                                                                                                                                                                                                          DTLYSCVV
                                                                                                                                                                                                                                                               SGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPS--VFLFPPKPKDTL
                                                                                                                                                                                                                                                                                                             VCLATNFTPTHI-----VIKWLKNGNQTTEGVRVEEPVEDKKRGYEATSYLSITRKEWDL
                                                                                                                                                                                                                                                                                                                                                       FGLTAN-SDTHLLQGQSLTLTLESPPGSSPSVQCRSP---RGKNIQGGKTLSVSQLELQD
                                                                                                                                                                                                                                                                                                                                                                                                     AVWD--NIEQFYCNAKHLDT---IKSVELKKDPVKPVEKPVVSIHPPSKDALALNESLFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GESMDPVTIGCLAKDFLPETISFTWGDKNNASYSTGLKSYKPVMQSSGTYSASSQVNVAS
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587 AA; 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77;
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7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
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PVLDSDGSFFLYSKLTVDKSRWQQ
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  404
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RESULT
Q7Z379
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Best Local S
Matches 135
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Q7Z379;
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Hypothetical protein DKFZp686K04218 (Fragment).
DKFZP686K04218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
NON_TER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Human rectum tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBI_TaxID=9606;
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                                                                              375
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460
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                                                                 NYKTTPPVLD-SDG--SFELYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                    I-VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
                                                                                                                                                                                                                                                                                           SPPGSSPSVOCRS-PRGKNIQGGKTLSVSQLEL----QDSGTWTCTVLQNQKKVEFKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHLLLVLQLALLP-----AATQGNKVVLGKKGDTVELTCTASQKK--SIQFHWKNSNQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDSFSCVVGHESLPLQLTQRSIDKSSGKPTNVNVSLVLSDTC 587
KPTHVNVSVVMAEVDGTC
                                                                                                                                                            ATFTWTPSSGK--SAVQGPPERDLCGCYSVSSVLPGCAQPWNHGETFTCTAAHPELKTPL
                                                                                                                                                                                   VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
                                                                                                                                                                                                                 VTVPCPVPPPPPC-----C----HPRLSLHRPALED-LLLGSEANLTCTLTGL-RDASG
                                                                                                                                                                                                                                                                   E---SGQNVTARNFPPSQDASGDLYTTSSQLTLPATQCPDGKSVTCHVKHYTNPSQ----D
                                                                                                                                                                                                                                                                                                                                                ----EVEDOKEEVQL-----LVFGLTANSDTH------LLQG----QSLTLTLE
                                                                                                                                                                                                                                                                                                                                                                            PGRGLEWMGYIYYSGSTYYNPSLESRLSISIDTSKNQFSLRLNSLTAADTAVYFCARGVG
                                                                                                                                                                                                                                                                                                                                                                                                   KILGNQ--GSFLTKGPSKLNDRADSRRSL---WDQGNFPLIIKNLKIEDSDTYIC----
                                                                                                                                                                                                                                                                                                                                                                                                                                 KHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSQTLSLTCTVSGGSIGSGDYFWSWIRQA
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                                                   KYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVSHEALPLAFTQKTIDRLAG
                                                                                                                                                                                                                                                                                                                       LGTAFDIWGQGTVVTVSSASPTSPKVFPLSLDSTPQDGNVVVACLVQGFFPQEPLSVTWS
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                       -----LQLDETC
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477
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Pred. No. 4.4e-19;
5; Mismatches 210
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RESULT 55
Q99LA6
ID Q99LA
AC Q99LA
DT 01-JU
DT 01-JU
DT 01-OC
DT 11-OC
DT Hypot

Q99LA6 PRELIMINARY; Q99LA6; 01-JUN-2001 (TrEMBLrel. 17, C 01-JUN-2001 (TrEMBLrel. 17, L 01-OCT-2003 (TrEMBLrel. 25, L Hypothetical protein.

Created) Last sequ Last anno

sequence update) annotation updat

484

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Q7237
AC Q7237
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DT 01-00
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DE HYPOT
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Best Local S
Matches 131
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Q7Z374;
01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W.,
Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenE
EMBL; BX538077; CAD98001.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
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DKFZP686C02218
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473
                        431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 11.9%; Score 322.5; DB 4
Similarity 26.3%; Pred. No. 5.9e-18;
31; Conservative 68; Mismatches 211
                                                                                                      SE---SGQNVTARNFPPSQDASGDLYTTSSQLTLPATQCPDGKSVTCHVKHYTNPSQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHLLLVLQLALLP-----AATQGNKVVLGKKGDTVELTCTAS----QKKSIQFHWKNSN
                                                   EKYLTWASRQEPSQGTTTPAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLA
                                                                    NNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                            GATFTWTPSSGK--SAVQGPPERDLCGCYSVSSVLPGCAQPWTHGETFTCTAAHPELKTP
                                                                                                                                                                                      EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                                                                                                                                                                          DI-VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
                                                                                                                                                                                                                                                                                                                           GPYGWFDPWGQGTLVTVSSASPTSPKVFPLSLDSTPQDGNVVVACLVQGFFPQBPLSVTW
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ĠKPTHVNVSVVMAEVĎGŤĊ
                      G-----LQLDETC
                                                                                                                                                                                                                  DVTVPCPVPPPPPC-----C----HPRLSLHRPALED-LLLGSEANLTCTLTGL-RDAS
                                                                                                                                                                                                                                                                                                  ESPPGSSPSVQCRS-PRGKNIQGGKTLSVSQLEL----QDSGTWTCTVLQNQKKVEFKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sec
(TrEMBLrel. 25, Last ann
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491
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RESULT
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AC Q99
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Best Local S
Matches 128
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InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 484 AA; 52567 MW;
Q99KA4 PRELIMINARY; PRT; 487 AA.
Q99KA4;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (PEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC003495; AAH03495.1; -. PIR; F33932; F33932. HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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128; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLQLALLPAATQGNKV------VLGKKGDTVELTCTASQKKSIQF--HWKNSNQIKI
                                                                                                                                             IDRLSG
                                                                                                                                                                                                                                                                                       DPEVKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNK
                                                                                                                                                                                                                                                                                                                                                                        VQCRSPRGKN-----IQGGKTLSVSQL----ELQDSGTWTCTVLQNQKKVE
                                                                                                                                                                                                                                                                                                                                                                                                                  VQLLVFGLTANSDTHLLQGQSLTLTLES------PPGSS------
                                                                                                                                                                                                                                                                                                                                                                                                                                     LKWMGWVNIETGESVYADDFKGRFAFSLETSASTIHLQINNLKNEDTATYFCARSDYDYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VWTLLFLMAAAQSIQAQIQLVQSGPELKKPGETVKISCKASGYTFTDYSMHWVKQAPGKG
                                                                                                                                                               LSLSPG
                                                                                                                                                                                                                                                                   EGAV-FTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHP
                                                                                                                                                                                                                                                                                                            -ELD-VNCSGPTPPPPITIPSCO----PSLSLQRPALED-LLLGSDASITCTLNGLRNP
                                                                                                                                                                                                                                                                                                                                 FKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
                                                                                                                                                                                                                                                                                                                                                     GTMNVTWGKSGKDITTVNFPPALASGGRYTMSSQLTLPAVECPEGESVKCSVQHDSNPVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                               431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.7%;
26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 315.5; DB 1
Pred. No. 2.2e-17;
7; Mismatches 200
       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8EAEA4F9BCF582FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91;
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                                                                                                                                                                                     459
                                                                                                                                                                                                                                                                                                                                                                                                                  152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
         RESULT 57
Q8VCX4
ID Q8VCX
AC Q8VCX
AC Q8VCX
AC J01-MA
DT 01-MA
DT 01-OC
DE Hypot
GN IGH-V
OS Muse T
OC Eukar
OC Mamma
OC NCBI
RN [1]
RN [1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 132;
                                     Hypothetical protein.
IGH-VU558 OR A1893585.
Mus musculus (Mouse).
Eukaryota; Metazoa; Cho
                                                                                       Q8VCX4 PRELIMINARY;
Q8VCX4;
01-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
                         NCBI_TaxID=10090;
         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg
                                                                                                                                                                                                                             386
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                                                                                                                                  PRELIMINARY;
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N.A

Chordata; Rodentia;

Craniata; Vertebrata; Sciurognathi; Muridae;

Euteleostomi;
; Murinae; Mus

20,

Created)

489 ₿

Last sequence update)
Last annotation updat

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 4.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 2.

Hypothetical protein.

SEQUENCE 487 AA; 52554 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BC004786; AAH04786.1;
HSSP; P01810; 2FBJ.
InterPro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007110; Ig-like
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MNRGVPFRHLLLVL---QLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHW---
                                                                                                                                                                                      QTPEKRLEWVATISDGGSY-TYYPDNVKGRFTISRDN-AKNNLYLQMSHLKSEDTAMYYC
SCMVGHEALPMNFTQKTIDRLSG
                                       SCSVMHEALHNHYTOKSLSLSPG 431
                                                                                 VRAFNPKEVLVRWLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAETWKQGDQY
                                                                                                                   VKGFYPSDIAVEWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVF
                                                                                                                                                               AERWNSGASFKCTVTHPESDT-LTGTIAKITVNTFPPQVHLLPPPSEELALNELVSLTCL
                                                                                                                                                                                                                                             LGSDASLTCTLNGLRNPEGAV-FTW----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGC
                                                                                                                                                                                                                                                                                     ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVL
                                                                                                                                                                                                                                                                                                                             CSVQHDSNAVQ-ELDVKCSGPPPPCP-PCPPSCH---
                                                                                                                                                                                                                                                                                                                                                                   CTVLQNQKKVEFKIDI-----VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLM
                                                                                                                                                                                                                                                                                                                                                                                                           GCLIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGGYTMS-SQLTLPAVECPEGESVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GKNIQ------GKNIQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ARDMGGSPYGGYSRFD---YWGQGTTITVSSESARNPTIYPLTLPRALSSDPVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV-QCRSPR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---- KNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.6%; Score 314.5; DB 11; 26.2%; Pred. No. 2.7e-17; :ive 76; Mismatches 188;
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                                                                                                                                                                                                                                                                                                                             PSLSLORPALED-LL
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RESULT

Q9 PP6

ID PP6

AC Q9

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Best Local Similarity
Matches 118; Conserv
                                                                                                                                                                                                                                                                                                              G9NPP6;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
Immunoglobulin heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC018322; AAH18322.1; -.
MGD; MGI:96486; Igh-VJ558.
Auffray C., Ansorge
Lehrach H., Poustka
"The European IMAGE
                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9NPP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 489 AA; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                         SEQUENCE FROM N.A.
                                                                                                                           Submitted
                                                                                                                                                    Pluvinet
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNFPPALASGGRYTMS-----SQLTLPAVECPEGESVKCSVQHDSNPVQELNVNCPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRSLWDQGNFPLI---IKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHL----LQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVKPGASVKLSCKASGYTESDYFTHWIKQRSGQGLEWIGWENPGS----GSIKFNEKFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKTIDRLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSPPTT---PPPPSCQPSLSLQRPALEDLLLGSDASITCTLNGL--RDPEGAVFTW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGGPSVFLFPPKPK------DTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH------TCPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GOSLTLTLESPPGSSPSV-----QCRS------PRG-KNI---QGGKTLSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GOGTLVTVSAEPAREPTIYPLTFPQALSSDPVIIGCLIHDYFPSGTMNVTWGKSGKDITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - PSTGKDAVOKKAVONSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-LTGTIAK
                                                                                                                         (JUL-2000) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
  e W., Ballabio A.,
a A., Lundeberg J
E consortium for :
                                                                                                                                                                                                                                               Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53208 MW;
                                                                                                                         to the EMBL/GenBank/DDBJ d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.6%; Score 313.5; DB 24.9%; Pred. No. 3.2e-17
               Ballabio A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70;
                                                                                                                                                                                                                                                                                                                      variant (Fragment).
                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC85B1194DAFEF2C CRC64;
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  integrated Molecular analysis
                                             Estivill X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             416
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                                                                                                                         oy L.;
databases
                                                  Gibson
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Best Local S
Matches 116
                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 4.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 3.

PROSITE; PS00290; IG MHC; 2.

NON TER 1

SEQUENCE 416 AA; 44786 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-2000) to the EMBL; AL389978; CAB97534.1; HSSP; P01789; 1MCP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human gene transcripts.";
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 116; Conserv
                                                   298
358
                         392
                                                                           338
                                                                                                       239
                                                                                                                                278
                                                                                                                                                          187
                                                                                                                                                                                    218
                                                                                                                                                                                                               136
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                                                                                                                                                                                                                                                                                             121
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                                                                                                                                                                                                                                                                                                                        19
                                                                                                                                                                                                                                                                                                                                                 78 DRADSRRSLWD-----QGNFPLIIKNLKIEDSDTYIC-----EVEDQKEEVQL----
                     YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG----
                                                 PPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAV
                                                                                                                                                                                                                                                                                  ----LVFGLTANSDTH------LLQG----QSLTLTLESPPGSSPSVQCRS-PRGKNI 163
                                                                                                                                                                                                                                                                                                                       TSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTC
                                                                PSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFL
                                                                                                      ERDLCGCYSVSSVLPGCAQPWNHGETFTCTAAHPELKTPLTANITKS-GNTFRPEVHLLP
                                                                                                                                                                                    ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
                                                                                                                                                                                                             SGDLYTTSSQLTLPATQCPDGKSVTCHVKHYTNPSQ---DVTVPCPVPPPPPC----C-
                                                                                                                                                                                                                                        QGGKTLSVSQLEL----QDSGTWTCTVLQNQKKVEFKIDI-VPCPAPEPKSCDKTHTCP
                                                                                                                                                                                                                                                                    PTSPKVFPLSLDSTPQDGNVVVACLVQGFFPQEPLSVTWSE---SGQNVTARNFPPSQDA
                                                                                                                               EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 337
                                                                                                                                                           ----HPRLSLHRPALED-LILGSEANLTCTLTGL-RDASGATFTWTPSSGK--SAVQGPP
                                                                                                                                                                                                                                                                                                                                                                          11.5%;
llarity 27.8%;
Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                 44786 MW;
                                                                                                                                                                                                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                                                                                          Score 312; DB 4;
Pred. No. 3.4e-17;
51; Mismatches 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                 8C41708BB8AB4687
                                                                                                                                                                                                                                                                                                                                                                             163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 databases
                                                                                                                                                                                                                                                                                                                                                                                                    Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                            78;
                       -LQLDETC
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 415
                         438
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                                                   357
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                                                                                                                                                                                                                                                                    135
                                                                                                                                                                                                                                                                                                                         78
                                                                                                         297
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RESULT 59
Q91WT1
ID Q91WT
  Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013490; AAH13490.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                    Q91WT1 PRELIMINARY;
Q91WT1;
Q1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
PROSITE; PS50835; IG_LIKE; PROSITE; PS00290; IG_MHC; Hypothetical protein.
                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                              TISSUE=Colon;
                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                Hypothetical protein. Mus musculus (Mouse).
                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                      Last sequence up
                                                                                                                                                                                                                                            Created)
                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                    481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8K172;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Similar to expressed sequence AI893585.
                                                                                                                                                                                                                                                                                                            Strausberg |
Submitted (
                                                                                                                                                                                                               EMBL;
PIR; F
PIR; F
PIR; F
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8K172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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mitted (APR-2002) to the E

L; BCC28249; AAH28249.1; -

33932; P33932; P33932;

H1105; PH1105; PH1105.

PH1108; PH1118.

PH1118; PH1118.

PH1119; PH1119.

PH1129; PH1125.

PH1126; PH1125.

PH1126; PH1125.

PH1136; PH1128.

PH1131; PH1131.

PH1131; PH1131.

PH1131; PH1131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTWGKSGKDITTVNFPPALASGGRYTMS-----SQLTLPAVECPEGESVKCSVQHDSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDRLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNG : ||:| | || : | | : : | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I---QGGKTLSVSQL--BLQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLTANSDTHLLQGQSLTLTLESPPGSSPSV-----QCRS------PRG-KN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVQLLQSGPE-----LVKPGASVKISCKASGYTFTSYYIHW-----VKQRPGQGLVWIGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESDT-LTGTIAKVTVNTFPPOVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEGAVFTW----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PE-VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVQELNVNCPGICSPPTT---PPPPSCQPSLSLQRPALEDLLLGSDASITCTLNGL--RD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----TCPELLGGPSVFLFPPKPK------DTLMISRTPEVTCVVVDVSHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -TRGGGWAFDYWGQGTTLTVSSEPAREPTIYPLTFPQALSSDPVIIGCLIHDYFPSGTWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFLTKGPSKLNDRADSRRSLW----DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52105
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                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 311; DB 11;
Pred. No. 5.1e-17;
7; Mismatches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97DF68D159463F65 CRC64;
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                                                                                                                                                                                                                                                                                                               databases
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PIR; PH1150; PH1150.

PIR; PH1151; PH1151.

PIR; PH1151; PH1151.

PIR; PH1152; PH1152.

PIR; PH1153; PH1153.

InterPro; IPR003197; Ig_cl.

InterPro; IPR003597; Ig_cl.

InterPro; IPR003596; Ig_wHC.

InterPro; IPR003596; Ig_w.

PERM; PF00047; Ig; 4.

SMART; SM00407; IGcl; 3.

SMART; SM00406; IGwHC.

PROSITE; PS50035; IG_MHC; 2.

SEQUENCE 482 AA; 52121 MW; A
                                                                                                                                                                                                                                                                                            Q91X92;
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01-DEC-2001
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TISSUB=Colon; Strausberg R.; Submitted (JUL-2001) to the EMBL; BC011181; AAH11181.1; PIR; F33932; F33932.

EMBL/GenBank/DDBJ

databases

SEQUENCE FROM N.A. NCBI_TaxID=10090;

Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

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RESULT
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS508290; IG_MHC; 2.
                                                                                            SEQUENCE FROM N.A.
STRAIN#11183, TISSUE=Blood;
MEDLINE=93329116; PubMed=8335933;
Gustafsson K., Germana S., Sundt '
"Extensive allelic polymorphion in
                                                                                                                                                                                                                                                                               CD4, allele 1 (Fragment).
Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                              Q29027
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Q19027;
Q1-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
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  miniature. . . ";
J. Immunol. 151:1365-1370(1993).
EMBL; X65629; CAA46583.1; - .
PIR; I47131; S21461.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GL--RDPEGAVFTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTH------TCPELLGGPSVFLFPPKPK-----DTLMISRTPEVTCVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLEWLGVIWTGGVTNYNSALKSRLSISKDNSKSOVFLKMNSLOTNDTARYYC-ARDSNYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYTOKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RWLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTVTHPESDT-LTGTIAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQHDSNPVQELNVNCPGICSPPTT---PPPPSCQPSLSLQRPALEDLLLGSDASITCTLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSGTMNVTWGKSGKDITTVNFPPALASGGRYTMS-----SQLTLPAVECPEGESVKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRG-KNI---QGGKTLSVSQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV-----QCRS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILGNQGSFLTKGPSKLNDRADSRRSL-WDQGNFPLIIKNLKIEDSDT--YICEVEDQKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LALLLCLVTFPSCAL-SQVQLKESGPDLVAPSQSLSITCTVSGFALTSYAISWVRQPPGK
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Last annotation updat
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AC Q9120
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DT 01-DE
DT Wyport
OS Mus T
OC Eukar
OC Mamma
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RN [1]
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Matches 59
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                      Matches 129;
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Strausberg R.;
Submitted (JUL-2001) to the EMB
EMBL; BC010324; AAH10324.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 486 AA; 52682 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF000476; Ig; 1.
SMART; SM00406; IGv; 1.
PROSTTE; PS50835; IG_LIKE; 1.
NON TER
99 99
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Q91Z07;
Q1Z07;
Q1-DEC-2001 (TrEMBLrel. 19,
Q1-DEC-2001 (TrEMBLrel. 19,
Q1-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                   185
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                                                                                                                                                                                                                                                                                                                                                          1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLG----KKGDTVELTCTAS--QKKSIQFHWK
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SVQHDSNAVQ-ELDVKCSGPPPPCP-PCPPSCH-----
                                                                         CLIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGGYTWS-SQLTLPAVECPEGESVKC
                                                                                                                                                            --VRPEIPIYYYSGSYFDS-----WGQGTTITVSSESARNPTIYPLTLPRALSSDPVIIG
                                                                                                                                                                                                  EDQKEEVQLLVF-GLTANSDTHLLQGQSLTLTLESPPGSSPSV-QCRSPR------
                                                                                                                                                                                                                                         RQTPERRLEWVAAITSGGNTYYPDNVKGRFTVSRDNAKYTLYLQMSSLKSEDTAMYYC---
                                                                                                                                                                                                                                                                               NSNQIKILGNQGSFLTKGPSKLNDRADSRRSL-WDQGNFPLIIK--NLKIEDSDTYICEV
                                                                                                                                                                                                                                                                                                                     MNFGL----RLIFLVLALKGVQCEVHLVESGGGLVKPGGSLKLSCVVSGFSFTSYDMSWV
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                                   TVLQNQKKVEFKIDI-----VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMI
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99 AA; 11170 MW;
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ilarity 25.7%;
Conservative 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52682 MW; 4FEF835125DA870B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  79;
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Last
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                                                                                                                                                                                                                                                                                                                                                                                                  Score 305; DB 11;
Pred. No. 1.6e-16;
9; Mismatches 188;
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PSLSLQRPALED-LLL
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\ Strauberg R.;

\ Submitted (JUN-2002) to the EMBL/GenBank/DDBJ dat Submitted (JUN-2002) to the EMBL/GenBank/DDBJ dat R EMBL; BC031703; AAH31703.1; -.

R InterPro; IPR003101; Ig-like.

R InterPro; IPR003596; Ig_MHC.

R InterPro; IPR003596; Ig_V.

R InterPro; IPR003596; Ig_V.

R InterPro; IPR003596; Ig_V.

R InterPro; IPR003596; Ig_V.

R Ffam; PF00047; Igc1; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00290; IG_MHC; 2.

SEQUENCE 488 AA; S3127 MW; 0E3B156E155733F0
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similar to expressed sequence AI893585.

Mus musculus (Mouse).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

MCBI_TaxID=10090;
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 LQLALLPAATQGNKVV------LGKKGDTVELTCTAS--QKKSIQFHW---KNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
EGESVKCSVQHDSNPVQELNVNCPGICSPPTT---PPPPSCQPSLSLQRPALEDLLLGSD
                                                                                                                                                                                                                                                                                                                 DYVDYSMD
                                                                                                                                                                                                                                                                                                                                                                EVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV-----QCRS-----
                                                                                                                                                                                                                                                                                                                                                                                                                          WIGRIDP -- NSGDTKFNEKFRTKATLTVDKPSSTVYMHLRSLTSEDSAVYYCTRRGLFYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILGNQGSFLTKGPSKLNDRADSRRSLW---DQGNFPLIIKNLKIEDSDTYIC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CMVGHEALPMNFTQKTIDRLSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGFYPSDIAVEWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLV
                                                                                                                                                                                                 GCLIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGRYTMS-----SQLTLPAVECP
                                                                                                                                                                                                                                                   -----PRG-KNI---QGGKTLSVSQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMLFLAAAATGVHSQVQLQQPGTELVKPGASVKLSCKASGYTFTSYWHWVKQRPGRGLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73;
                                                                                                                                                                                                                                                                                                           ----YWGOGTSVTVSSEPAREPTIYPLTFPOALSSDPVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 304; DB 1
Pred. No. 2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0E3B156E155733F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               467
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                                                                                                                                         -DTLMISRT
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RESULT
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                                                                                                                                                                                                                           Query Match
Best Local S
Matches 107
                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U18701; AAB48195.1; --
PIR; S60266; S60266.
HSSp; P01842; 2MCG.
GO; GO:0004872; F:receptor act:
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q90544
Q90544;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A new antigen receptor gene family that undergoes extensive somatic diversification in sharks."; Nature 374:168-173(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
Ginglymostomatidae; Ginglymostoma.
NCBI_TaxID=7801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel antigen receptor precursor Ginglymostoma cirratum (Nurse sha
                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                        SMART; SM00407; IGc1; 4.

PROSITE; PS50835; IG_LIKE; 6.

PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Greenberg A.S., Avila D., Hughes M., Hughes A., Flajnik M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=Spleen;
                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig;
SMART; SM00407; IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95183140; PubMed=7877689;
                                                                                                                                                                                                                                                                                                                             Receptor; Signal.
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                                                                                                                                                                                                                              107;
                                                                                                                                                                                                  37
                                                                                                                                                                                                                                          Similarity
                            PAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VKFN
                                                                                  CRSPRGKNIQGGKTLSVSQLELQDSGTWTCT------
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                                                                                                                                         IIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQ
                                                                                                                                                                    VEYTCSAKODOSSTPVVKRTRKARVEPTKPHLRLLPPSPEEIOSTSSATLTCLIRGFYPD
                                                                                                                                                                                          VELTCTASQKKSIQFHWKNSNQIKILGNQG--SFLTKGPSKLNDRADSRRSLWDQGNFPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGHEALPMNFTOKTIDRLSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FYPSDIAVEWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WNSGASFKCTVTHPESDT-LTGTIAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASITCTLNGL--RDPEGAVFTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAER
                                                                                                                                                                                                                                                                                     684 AA;
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                   19
                                                        ----LLNLTAVEWKSGAKYTCTASHPPSQSTVKRVIRNQ----
                                                                                                                                                                                                                                                                                   75224 MW;
                                                                                                                                                                                                                           11.2%; Score 301.5; DB 1
25.1%; Pred. No. 5.1e-16;
tive 66; Mismatches 161
                                                                                                               -SVSWOKDDVS--VSANVTNFPTAL--EQDLTFSTRS
                                                                                                                                                                                                                                                                                                                                                                                                                                            activity;
                                                                                                                                                                                                                                                                                   POTENTIAL.
NOVEL ANTIGEN RECEPTOR.
; 2FF9D2071CDA6DFD CRC64;
-SVSLLKP-PFEEIWTQQTATIVCEIV---YSDLENIKVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       shark)
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                                                                                                                                                                                                                                                     DB 13; Length
                                                                                                                                                                                                                            161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McKinney
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rearrangement
                                                                                 -VLQNQKKVEFKIDIVPC
                                                                                                                                                                                                                            92;
                                                        -KVD-
                                                                                                                Gaps
                            261
                                                        452
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                                                                                                               414
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Sin
Matches 121;
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01-DEC-2001 (TrEMBLrel. 19, Created o1-DEC-2001 (TrEMBLrel. 19, Last so o1-DEC-2001 (TrEMBLrel. 25, Last and Hypothetical protein (Fragment).
Mus musculus (Mouse).
Eukaryota Metazoa; Chordata; Cran.
Mammalia; Eutheria; Rodentia; Sciu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010798; AAH10798.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
NON_TER 1
SEQUENCE 480 AA; 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NFGLSLIFLVLILKGVLCDVKLVESGGGLVKPGGSLRLSCAASGFIFSNSYMSWVRQTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS-------QKKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVLSDT 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOLDET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKAK-GQPREPQVYTLPPSRDEL-TKNQVSLTCLVKGFYPSDIAVEWESNGQ-PENNYKT
                                                                                                                                                                                                                                                                                                                                           CEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV-----QCRS-----
                                                                                                                                                                                                                                                                                                                                                                                                                     KRLEW-----VATISNSG-YATHYPDSMKGRFTISRDN-AQNTVLLQMTSLNSEDTAVYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVDSEKGSGSSFVTDRLRLTAAEWNSDTTYSCLVGHPSLNRDLIRSTNKSNGKPSSVNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WQVNGVERKKGVETQNPEWSGSKSTIVSKLKVMASEWDSGTEYVCLVEDSELPTPVKASI
DASITCTLNGL--RDPEGAVFTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAE
                                              TPEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQ
                                                                                                                                                   PAPEPKSCDKTH-----TCPELLGGPSVFLFPPKPK-----
                                                                                                                                                                                                             IGCLIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGRYTMS-----SQLTLPAVEC
                                                                                                                                                                                                                                                         -----prg-kni----QGGKTLSVSQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH-----NHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
                                                                                                  PEGESVKCSVOHDSNPVQELNVNCPGICSPPTT---PPPPSCQPSLSLQRPALEDLLLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51936 MW; 20B9234EEF2B41ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.1%; Score 300.5; DB 1
24.2%; Pred. No. 3.7e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                  -----VWGAGTTVTVSSEPAREPTIYPLTFPQALSSDPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11; Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200;
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                                                                                                                                                         -----DTLMISR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                     268
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DE Hypot
OC Eukaa
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Sim
Matches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MCC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 494 AA; 53088 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Mammary gland;
Ileogai T., Otta T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Ileogai T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara N.
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi (
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.;
"MEDO human CDNA sequencing project.";
"MEDO human CDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         096K68;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein FLJ14473.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AK027379; BAB55072.1; -. PIR; S21205; S21205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q96K68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
253
                                  213
                                                                                                                176
                                                                                                                                                      133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVK
PSTPPTPSPSCCHPRLSLHRPALED-LLLGSEANLTCTLTGL-RDASGVTFTWTPSSGK-
                                  THTCPELLGG---PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
                                                                      NFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCPVPSTPPTPS
                                                                                                                                                                                          QSLTLTLESPPGSSPSV----QCRSPRGKN-----IQG---GKTLSVSQLE-----
                                                                                                                                                                                                                                  S-RDNAKNSLYLQMN----
                                                                                                                                                                                                                                                                                                           LVKPGGSLRLSCAASGLSFSTYAMNWVRQAPGKGLEWVSSISSRSDYIYYRDSVKGRFTI
                                                                                                                                                                                                                                                                                                                                               LGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKILGNQGSFL-----TKGPSKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFNPKEVLVRWLHGNEELSPESYLVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFYPSDIAVEWESNGQ---PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RWNSGASFKCTVTHPESDT-LTGTIAKVTVNTFPPQVHLLPPPSEELALNELLSLTCLVR
                                                                                                                                                      QGTLVTVSSASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTAR
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53088 MW; 9A1D7AEB5AEE4C0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     11.1%;
                                                                                                                                                                                                                                                                                                                                                                                   ; Score 300.5; DB 4; ; Pred. No. 3.9e-16; 71; Mismatches 193;
                                                                                                                                                                                                                                  ---SLRVDDTAVYYCARDSCNGAI---CYGFSP-----WG
                                                                                              -TWTCTVLQNQKKVEFKI------DI-VPCPAPEPKSCDK
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                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 121
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01-DEC-2001
01-DEC-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013488; AAH13488.1; -.
MGD; MGI:96486; Igh-VJ558.
InterPro; IPR007110; Ig-like.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
IGH-VJ558 OR AI893585.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                              Hypothetical protein 
SEQUENCE 481 AA; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q91WT3
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                          216
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 244
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                                                                                                                                                                                                                                                                 16
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                                                                                                                                                                                                                                                                                         Similarity 24.3
21; Conservative
                                                                                                                                                                                                                                                            LALLPAATQGNKVV-----LGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQG-
                                                                                                                                                                                                                                     QTTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMA
VTCVVVDVSHEDPE-VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWL
                                                                                                                                             EDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV-----QCRS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVDGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-S
                        ESVKCSVQHDSNPVQELNVNCPGICSPPTT---PPPPSCQPSLSLQRPALEDLLLGSDAS
                                                                              LIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGRYTMS-----SQLTLPAVECPEG
                                                                                                    ----PRG-KNI---QGGKTLSVSQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAP
                                                                                                                                                                                    EWIGAIDPFDSYTSYNQKFKGTTLTVDTSSS-----SAYMLLSSLTSEDSAVYFC--
                                                                                                                                                                                                            -----SFLT-----KGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLDETC 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG------L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SAVQGPPERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKS-GNTF
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1 (TremBLrel. 19,
3 (TremBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               493
                                                                                                                                                                                                                                                                                                   11.0%;
                                                                                                                              --ARGPRDSSGYYWGQGTTLTVSSEPAREPTIYPLTFPQALSSDPVIIGC
                                                                                                                                                                                                                                                                                                                                               52022 MW;
                                                  ----TCPELLGGPSVFLFPPKPK-----
                                                                                                                                                                                                                                                                                           69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                         Score 298.5; DB 11; Length 481;
Pred. No. 5.5e-16;
9; Mismatches 183; Indels 125;
                                                                                                                                                                                                                                                                                                                                            4EEB5C253038B718 CRC64;
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                                                                                                                                                                                                                                                                                         Indels 125;
                                                  ----DTLMISRTPE
                                                                                                                                                                                                                                                                                         Gaps
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Best Local Similarity
Matches 111; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (DEC-2001) to the EMI EMBL; BC019425; AAH19425.1; -. MGD; MGI:96486; Igh-VJ558. InterPro; IPR0077110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR00396; Ig_V. Pfam; PF00047; ig; 4. SMART; SM00406; IGV; 1. PROSITE; PS50835; IG_LIKE; 4. PROSITE; PS50835; IG_LIKE; 4. PROSITE; PS508290; IG_MHC; 2. HYDOTHETGAT
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QBVEAO;
QBVEAO;
QBVEAO;
QBVEAO;
Q1-MAR-2002 (TrEMBLrel.
Q1-MAR-2002 (TrEMBLrel.
Q1-OCT-2003 (TrEMBLrel.
Hypothetical protein.
IGH-VJ558 OR AI893585.
Mus musculus (Mouse).
Eukaryota; Metazoa; Choi
Mammalia; Eutheria; Rode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (DEC-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                      163
                                                                                                                                                                                                                                                                                                                                                                                                                                          118 ARAYSNYYFDNWGQGTTLTVSSEPAREPTIYPLTFPQALSSDPVIIGCLIHDYFPSGTMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 LTANSDTHLLO-GOSLTLTLESPPGSSPSV-----OCRS------PRG-KN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65
ESDT-LTGTTAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGN
                                                   ALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNO-VSLTCLVKGFYPSDIAVEWESNG
                                                                                                                                         PE-VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNK 311
                                                                                                                                                                                                                   PVQELNVNCPGICSPPTT---PPPPSCQPSLSLQRPALEDLLLGSDASITCTLNGL--RD
                                                                                                                                                                                                                                                                                                                             VTWGKSGKDITTVNFPPALASGGRYTMS-----SQLTLPAVECPEGESVKCSVQHDSN
                                                                                                                                                                                                                                                                                                                                                                                 I---QGGKTLSVSQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGRFTI-----SRDNSQNILYLQMN-----TLRAEDSATYYC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGASFKCTVTHPESDT-LTGTIAKVTVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFN
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                                                                                                                                                                                                                                                                          -----TCPELLGGPSVFLFPPKPK------DTLMISRTPEVTCVVVDVSHED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             484 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52859 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.0%; Score 297.5; DB 1
26.1%; Pred. No. 6.7e-16;
cive 56; Mismatches 154
                                                                                                         EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56;
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Last sequence update)
Last annotation update)
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Best Local S
Matches 118
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InterPro; IPR003599; Ig. ...
InterPro; IPR003599; Ig. G.1.
InterPro; IPR003597; Ig. G.1.
InterPro; IPR003006; Ig. MHC.
InterPro; IPR003596; Ig. V.
Pfam; PF00047; Ig; 3.
SMART; SM00409; IG; 3.
SMART; SM00407; IGC1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG. LIKE; 4.
PROSITE; PS50835; IG. MHC; 2.
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Q80ZI7;
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Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein SEQUENCE 487 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                      320
                                                                                 297
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18; Conservative
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                                  TISKAKGOPREPOVYTLPPSRDELTKNO-VSLTCLVKGFYPSDIAVEWESNGO---PENN
                                                                                                                                                                                                                                              DITTVNFPPALASGGRYTMS-----SQLTLPAVECPEGESVKCSVQHDSNPVQELNVN
                                                                                                                                                                                                                                                                                       TLSVSQL--ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH-----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVQPGGSMKLSCAAS-GFTFSNYMMNWVRQSPEKGLEWVAEIRLRSN--NYATHYAESVK
TIAKVTVNTEPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESY
                                                                                                                      YVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 319
                                                                                                                                                                                                        CPELLGGPSVFLFPPKPK------DTLMISRTPEVTCVVVDVSHEDPE-VKFNW
                                                                                                                                                                                                                                                                                                                                  FDVWGAGTTVTVSSEPAREPTIYPLTFPQALSSDPVIIGCLIHDYFPSGTMNVTWGKSGK
                                                                                                                                                                                                                                                                                                                                                                     HLLQGQSLTLTLESPPGSSPSV-----QCRS------PRG-KNI---QGGK 167
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                                                                                                                                                               CPGICSPPTT---PPPPSCQPSLSLQRPALEDILLGSDASITCTLNGL--RDPEGAVFTW
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24.7%; Pred. No. 6.7e-16;
7ative 72; Mismatches 173
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Last annotation update)
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AC Q96KO
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OC Mamma
OC NCBI
RR [1] ""
RN [1] ""
RN [1] ""
RN [1] ""
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Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCC016369; AAM16369.1; -.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003596; Ig_v.
R Pfam; PP00047; ig; 4.
R Pfam; PP00047; ig; 4.
R SMART; SM00406; IGv; 1.
R PROSITE; PS05035; IG_LIKE; 4.
R PROSITE; PS05035; IG_LIKE; 4.
R PROSITE; PS05035; IG_MHC; 1.
W Hypothetical protein.
Q SEQUENCE 496 AA; 53391 MW; D346929849040D69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 131;
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Q96KX8, PRELIMINARY,
Q196KX8, Q100 (TEMBLrel 19,
01-DEC-2001 (TEMBLrel 19,
01-DCT-2003 (TEMBLrel 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKTIDRLSG
                                                                                                                                                                                           VSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QIKILGNQGSFLTKGPSKLNDRADSRRSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQ 114
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TQKTIDRLAGKPTHVNVSVVMAEVDGTC
                                      TOKSLSLSPG------LQLDETC
                                                                           LQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAF
                                                                                                                                                                 AAYPESKTPLTATLSKS-GNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRW
                                                                                                                                                                                                                                                LTGL-RDASGVTFTWTPSSGK--SAVQGPPERDLCGCYSVSSVLPGCAEPWNHGKTFTCT
                                                                                                                                                                                                                                                                                         VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK
                                                                                                                                                                                                                                                                                                                                  YTNPSQDVTVPCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALED-LLLGSEANLTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HILLUAAPRWVLSQLQLQESGPGLVKSSETLSLTCTVSGGSISSSSYYWGWIRQP
                                                                                                                    ESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
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; Pred. No. 6.9e-16;
60; Mismatches 226
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Best Local Similarity
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InterPro; IPR00359; Ig. 1ke.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig.MC.
InterPro; IPR003056; Ig.v.
PF00047; Ig; 4.
SMART; SM00400; IG; 4.
SMART; SM00407; IGc1; 2.
SMART; SM00407; IGc1; 2.
SMART; SM00406; IGv16.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Mammary gland;
Iroogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.
Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
Wasuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
"NEDO human cDNA sequencing project.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO74651, BAC11114-1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Hypothetical protein FLJ90170.
Homo Bapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Primates; Catarrhini; Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein SEQUENCE 493 AA;
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01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                         GPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT
SRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVN
                                                                                                                                                                                                                                                                        ---RSPRGKNIQGGKTLSVSQLELQDS-----GTWTCTVLQNQKKVEFKIDI-VPCPAPE
                                                                                                                                                                                                                                                                                                        HWGQGTLVTVSSASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGV
                                                                                                                                                                                                                                                                                                                                     HLLQGQSLTLTLESP------PGSSPSVQC------
                                                                                                                                                                                                                                                                                                                                                                     GRLTVS-RDNYKNTLY-----LEMKSLGAEDTAVYYC-ARDQ----GYAGYGVF----D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNSNQ-----IKILGNQG-----SFLTK
                         PVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG-----
                                                                                                                        PSSGK--SAVQGPPERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSK
                                                                                                                                                   VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK
                                                                                                                                                                                 TPPTPSPSTPPTPSPSCCHPRLSLHRPALED-LLLGSEANLTCTLTGL-RDASGVTFTWT
                                                                                                                                                                                                              PKSCDKTHTCPELLGG----PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
                                                                                                                                                                                                                                              TARNEPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQ----DVTVPCPVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGVVL--PGGSLRLSCAASGFRFRDYDMHWVRQSPGEGLEWVALIWYDGTKTYYSDSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.9%; Score 295; DB 4; I larity 25.4%; Pred. No. 1.1e-15; Conservative 67; Mismatches 196;
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Best Local Sim
Matches 113;
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EMBL; BC013539; AAH13539.1; -.

RMGD; MGI:96486; Igh-VJ558.

InterPro; IPR0077110; Ig-like.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.

Ffam; pP00047; ig; 4.

SMART; SM00406; IGv; 1.

PROSITE; PS00209; IG_MHC; 2.

Hypothetical protein.

SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;
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Q91WR1;
01-DEC-2001
01-DEC-2001
01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein. IGH-VJ558 OR AI893585. Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 LVKPGASVKLSCKASGYTITDYYVNWVKQSHGKSLEWIGDINPY--NGGTSYNQKFKGKA
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EGATTYLVTSVLRVSAEIWKOGDOYSCMVGHEALPMNFTQKTIDRLSG
                                DG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                     PPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFEPLKEPG
                                                                                                                                         EPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ----PENNYKTTPPVLDS
                                                                                                                                                                                                                KDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-LTGTIAKVTVNTF
                                                                                                                                                                                                                                                               KTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR
                                                                                                                                                                                                                                                                                                                      ---PPPPSCQPSLSLQRPALEDLLLGSDASITCTLNGL--RDPEGAVPTW-----
                                                                                                                                                                                                                                                                                                                                                                          FLFPPKPK----
                                                                                                                                                                                                                                                                                                                                                                                                                            LASGGRYTMS-----SQLTLPAVECPEGESVKCSVQHDSNPVQELNVNCPGICSPPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH-----TCPELLGGPSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.8%; Score 293; DB 11; 24.1%; Pred. No. 1.6e-15; cive 73; Mismatches 188;
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BC032249; AAH32249.1; -.

R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003006; Ig.MC.
R InterPro; IPR003596; Ig.WC.
R InterPro; IPR003596; Ig.V.
R Ffam; PR00047; Ig. 4.
SWART; SW00407; IG.; 4.
SWART; SW00407; IG.; 2.
SWART; SW00407; IG.; 1.
SWART; SW00406; IG.; 1.
SWART; SW00406; IG.; 1.
SWART; SW00406; IG. LIKE; 4.
PROSITE; PS50835; IG.LIKE; 4.
PROSITE; PS50835; IG.MHC; 1.
WHYPOTHETICAL PROTECTION.
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Best Local S
Matches 129
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Q8N5K4;
01-OCT-2002
01-OCT-2002
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                                                                                                                                                                                                                                                                                                                          NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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HVNVSVVMAEVDGTC
                                                                                                                                                                                                                                                                                                                                                                                      VPSTPPTPSPSTPTPSPSCCHPRLSLHRPALED-LLLGSEANLTCTLTGL-RDASGVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                      APEPKSCDKTHTCPELLGG---PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D-----VWGKGTTVTVSSASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSDTHLLQGQSLTLTLESPPGSSPSV----QCRSPRGKN-----IQG---GKTLSVSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSVKGRFTIS-RDNAKNSLYLQMN-----SLRVEDTALYYCARDPTKYCSGGSCLGYYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTA
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                                                                                            TWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPT
                                                                                                                                                                                                                                                                                         TWTPSSGK--SAVQGPPDRDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESGQGVTARNFPPSQDASGDLYTTSSQLTLPATQCLAGKSVTCHVKHYTNPSQDVTVPCP
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Pred. No. 2.
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Matches 126
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SMART; SM00406; IGv; 1.

SMOSITE; PS50835; IG LIKE; 4.

PROSITE; PS50835; IG_MHC; 1.

Hypothetical protein.

SEQUENCE 496 AA; 53532 MW;
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Q96DK0;
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01-DEC-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens (Human).
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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VDGTC
                                                  LDETC 438
                                                                                                          GTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAE
                                                                                                                                                                                                                        SAVQGPPDRDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKS
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                                                                                                                                                                G--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG------LQ
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(TrEMBLrel. 19, Last sequence up
(TrEMBLrel. 25, Last annotation
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Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
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A Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
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A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storich K.-F.,
A Sasaki H., Sato K., Kang K.H., Weitz C., Whittaker C., Wilming L.,
A Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
Adult male kidney cDNA, RIKEN full-length enriched library,
clone:0610041A01, full insert sequence.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; 1g; 4.

SMART; SM00407; IGc1; 2.

PROSITE; PS50835; IG_LIKE; 3.

PROSITE; PS00290; IG_MHC; 2.

SEQUENCE 426 AA; 45819 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001).
EMBL; AK002875; BAB22422.1; -.
PIR; F33932; F33932.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9DCD9
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
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                              285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                      IKNIKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESP-----PGS
--YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                        SLORPALED-LILGSDASLTCTLNGLRNPEGAV
                                                                                                                                                            PAVECPEGESVKCSVQHDSNAVQ-ELDVKCSGPPPPCP-PCPPSCH-----PSL
                                                                                                                                                                                                                                                   LPRALSSDPVIIGCLIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGGYTMS-SQLTL
                                                                                                                                                                                                                                                                                                                                            LSSLTSEDSAVYFCARSDYYGPYAMDYWG-----QGTSVTVSSESARNPTIYPLT
                                                                                                                FLF PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST-
                                                                                                                                                                                                         ---ELODSGTWTCTVLQNQKKVEFKIDI-----VPCPAPEPKSCDKTHTCPELLGGPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.6%; Score 286.5;
26.8%; Pred. No. 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 4.5e-15
8; Mismatches 14
                                                                                                                                                                                                                                                                                                  56E1275BA48F6FB1 CRC64;
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Best Local S
Matches 126
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 479 AA; 51603 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q91WP5;
Q91WP5;
01-DEC-2001
01-DEC-2001
01-OCT-2003
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
VQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-LTGTIAKVTVNTFPPQ
                                                                                                                                                                                                                                                                                                                                         QGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCP-----APEPKSCDKTHTC
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                                                                                                                                                                                      ----PSLSLQRPALED-LLLGSDASITCTLNGL--RDPEGAVFTW-----
                                                                                                                                                                                                                                      PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VKFNWYVDGVEVHNAKTK
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                                                                                                                                   PREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
                                                                                                                                                                                                                                                                                                                                                                                         CLIHDYFPSGTMNVTWGKSGKDIT-TVNFPPALASGGRYTMSSQLTLPAVEC--PEGESV
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1 (TrEMBLrel. 19,
3 (TrEMBLrel. 25,
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Rodentia;
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                                                                                                                                                                                                                                                                                      ----CSVQHDSNPVQ-ELN-VNCPGICSPPTTPPPPSCQ-----
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Last annotation update)
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Pred. No. 5.3e
90; Mismatches
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Stapleton M., Journ T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Bosak S.A., McEwan P.J., McKernan K.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Mitting M., Madan A., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Korpe G. J. Maryan M. S., Schmutz J., Myers R.M., Schein J.E.,

Korpe G. J. Maryan M. S., Schmutz J., Schmerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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Q7TMK4;
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-C57BL/60; TISSUE-Breast tumor;
MEDLINE-22388257; PubMed-12477932;
MEDLINE-22388257; PubMed-12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases EMBL; BC055905; AAH55905.1; -.
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Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 479 AA; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000
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201
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117; Conserv
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  PCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                    WGKSGKDITTVNFPPALASGGRYTMSSQLTLPAVECPEGESVKCSVQHDSNPVQ-ELD-V
                                                                                                                    -----DYWGRGISVTVSSESARNPTIYPLTLPPALSSDPVIIGCLIHDYFPSGTMNVT
                                                                                                                                                                                                  --GRFTI-----SRDDSKSGVYLQMN-----NLRPEDMGIYYCTVEGM------
                                                                                                                                                                                                                                     NQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF
                                                                                                                                                                                                                                                                          LVQPGRPMKLSCVASGFTFGDYWMNWVRQSPEKGLEWVSQIRNKPYNYETYYSDSVK---
                                                                                                                                                                                                                                                                                                                   LGKKGDTVELTCTAS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                      52209 MW;
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                                                                         ---IQGGKTLSVSQL-----ELQDSGTWTCTVLQNQKKVEFKIDIV
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                             Score 284.5; DB Pred. No. 7.7e-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                      532DED9D46D0AEED CRC64;
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                                                                                                                                                                                                                                                                                                                                                          168;
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Q8VCV

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Best Local Similarity
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OBVCV5;
OL-MAR-2002 (TrEMBLrel. 20
OL-MAR-2002 (TrEMBLrel. 20
OL-OCT-2003 (TrEMBLrel. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (DEC-2001) to the ENEMBL, BC018455, AAH18455, I, InterPro, IPR007110, Ig_like. InterPro, IPR003006, Ig_MiC. InterPro, IPR003596, Ig_vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein SEQUENCE 481 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 4. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG_LIKE; PROSITE; PS00290; IG_MHC; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                     DAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPE-SGTLTGTIAKVTVNTFP
                                                                                                       TKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE
                                                                                                                                                                                                                     HTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK
                                                                                                                                                                                                                                                                          PPALASGGRYTMSSQLTLPAVECPEGESVKCSVQHDSNPVQ-ELD-VNCSGPTPPPPITI 248
                                                                                                                                                                                                                                                                                                                                                                               TLVTVSAESARNPTIYPLTLPPALSSDPVIIGCLIHDYFPSGTMNVTWGKSGKDITTVNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVRPGTSVKVSCKASGYSFIDYNIYWVKQSHGKSLEWIGYIDPYNGGSSYNQKFKGKATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILG-----NQGSFLT---KGPSKL
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                                                                                                                                                                PSCQ----PSLSLQRPALED-LLLGSDASITCTLNGLRNPEGAV-FTW-----EPSTGK
                                                                                                                                                                                                                                                                                                                                                                                                                                        QSLTLTLES-----
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                                                                                                                                                                                                                                                                                                                          ----IQGGKTLSVSQL-----ELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.5%; Score 284.5; DB 1
25.5%; Pred. No. 7.8e-15;
Live 67; Mismatches 182
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RESULT
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A Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
T "Identification and characterization of SNC66, a Ig-like gen
down-regulated in colorectal cancer.";
L Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL; AF283666; AAL36987.1; -.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR003006; Ig_MHC.
R InterPro; IPR003096; Ig_WHC.
R InterPro; IPR003596; Ig_V.
R Pfam; PF00047; 1g; 4.
R PfSMTTE; PS00185; IG_IIXE; 4.
R PROSITE; PS00290; IG_MHC; 1.
R PROSITE; PS00290; IG_MHC; 1.
R PROSITE; PS00290; IG_MHC; 1.
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Matches 129; Conserv
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Mammalia, Eutheria,
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                                                                                                                                                                                                                                                                                                                                                                            NQKKVEFKIDI-VPCPAPEPKSCDKTHTCPELLGG---PSVFLFPPKPKDTLMISRTPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- QSLTLTLESPPGSSPSVQCRS-PRGKNIQGGKTLSVSQLELQDS-----GTWTCTVLQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGLEWMGWMNPQTGNTEFAQKFQGRLTFSRDT----SINTAYMVLSSLSTEDSAIYFCA 116
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                                                VRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALP
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_MHC.
Pfam; PF00047; ig; 3.
SWART; SW00407; IGcl; 2.
SWART; SW00407; IGcl; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS500290; IG_MHC; 1.
SEQUENCE 384 AA; 40947 MW;
Q99M22
Q99M22;
01-JUN-2001
01-JUN-2001
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01-OCT-2003
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ
EMBL; AF067420; AAC19365.1; -
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Zheng S., Cao J., Cao W., Cai X., Ger
"Identification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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  (TrEMBLrel.
                                                                      PRELIMINARY;
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Best Local Similarity
Matches 115; Conserv
Q29028 PRELIMINARY; P. Q29028; O1-NOV-1996 (TrEMBLrel. 01, Cre. 01-NOV-1996 (TrEMBLrel. 25, Las. CD4, allele 2 (Fragment). Sus scrofa (Pig). Eukaryota; Metazoa; Chordata; C.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS508290; IG_MHC; 2.
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002091; AAH02091.1; -.
HSSP; P01810; 2FBJ.
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Mus musculus (Mouse).
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                       VQHDSNPVQ-ELD-VNCSGPTPPPPITIPSCQ-----PSLSLQRPALED-LLLGSDASIT
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479 AA; 51
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    Craniata;
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Sciurognathi;
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    Vertebrata; Euteleostomi;
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chi; Muridae; Murinae; Mus
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InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS0035; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 500 AA; 54154 MW;
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SEQUENCE
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005951; AAH05951.1; -.
HSSP; P01789; 1MCP.
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STRAIN#11183, TISSUE=Blood;
MEDLINE=93329116; PubMed=8335933;
Gustafsson K., Germana S., Sundt T.M.,
"Extensive allelic polymorphion in an
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2003 (TrEMBLrel. 25,
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PIR; 17132; S21462.
HSSP; P01730; 1CDY.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGv;
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                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGP-SKLNDRADSRRSLWDQG
                                                                                                                                                 86 LWDQGN---
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                                                                      VWGKGTTVTVSSASPTSPKVFPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGV
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                                                                                                                                                                                                                               Conservative
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--ANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLEL
                                                                                                                                                                                                                                                                                                                                                                                54154 MW; 0A9BF43F2A3CC6D9 CRC64;
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56.1%; Pred. No. 1.8e-15;
tive 19; Mismatches 23
                                                                                                                                                 ----FPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF-----GL
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Last annotation updat
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                                                                                                                                                                                                                       Score 273.5; DB 4;
Pred. No. 6.6e-14;
6; Mismatches 154;
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Best Local (
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InterPro; IPR003599; Ig.
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InterPro; IPR003597; Ig.cl.
InterPro; IPR003596; Ig.MHC.
InterPro; IPR003596; Ig.MHC.
INTERPRO; IPR003596; Ig.y.
PEam; PF000407; Ig.; 4.
SWART; SW00409; IG; 3.
SWART; SW00400; IGv; 1.
PROSITE; PS50835; IG.MHC; 2.
SEQUENCE 480 AA; 51645 MW; 8
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to expressed sequence AI893585.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC029188; AAH29188.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                LGKKGDTVELTCTAS -- QKKSIQFHWKNSNQIKILGNQG----SFLT--KGPSKLNDRAD
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                                                                                                                                                                                          GKATLTADKSSNTAYMHLSSLTSENSAVYFC-----ARSKLGGFAYWG
                                                                                                                                                                                                                                      SRRSLW----DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSD----THLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLARGESPKÖVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLTVDKSRWQQGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAEPWNHGKTFTCTAAYPESKTPLTATLSKS-GNTFRPEVHLLPPPSEELALNELVTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ED-LLLGSEANLTCTLTGL-RDASGVTFTWTPSSGK--SAVQGPPDRDLCGCYSVSSVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
                                                                                QGTLVTVSAESARNPTIYPLTLPPALSSDPVIIGCLIHDYFPSGTMNVTWGKSGKDITTV
                                                                                                                                                                                                                                                                                              LVKPGALVKISCKASGYTFTSFDISW-----MKQRPGQGPEWIGWISPGDGSSEYNEKFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TCHVKHYTNPSQ---DVTVPCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QDSGTWTCTVLQNQKKVEFKIDI-VPCPAPEPKSCDKTHTCPELLGG---PSVFLFPPKP
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                 10.0%;
                                                                                                                                                                                                                                                                                                                                                                                                        71;
                                                                                                                                                                                                                                                                                                                                                                                                  Score 270; DB 11;
Pred. No. 1.2e-13;
'1; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8690A63C669CDBED CRC64;
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Best Local S
Matches 129
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Q8WU38;
01-MAR-2002
01-MAR-2002
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021276; AAH21276.1; -.
PIR; S21205; S21205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein 
SEQUENCE 573 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
285 YRVVSVLTVLHQDWLNGKEYKCKVSN--
                                                                                                                                                                                                              165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129;
                                                                                                                                                                                                                                                                                                                                                                           58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MNRGVPFRHLLLVL---QLALLPAATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 21.3%;
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                                                                                                    VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST
                                                                                                                                                                                                            GGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPS
                                                                                                                                                                                                                                                                      ALYYCAKHGSGSYI----
                                                                                                                                                                                                                                                                                             DTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQ 164
                                                                                                                                                                                                                                                                                                                                                                           QAPGKGLEWVSGISWNSGSIGYADSVKGRFTIS-RDNAKNSLYLQMN-----SLRAEDT
                                                                                                                                                                                                                                                                                                                                                                                                                           SNQIK-----ILGNQGSF----LTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MELGLSWIFLLAILKGVQCEVQLVESGGGLV---QPGRSLRLSCAASGFTFDDYAMHWVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62967 MW; FD072344033AC530 CRC64;
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                                                                                                                                                            -----FPI-ISGCRHPKDNS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65;
                                                                                                                                                                                                                                                                    -GYYYGMD----VWGQGTTVTVSSAPTKAPDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                     LACLI - - TGYHPTSVTVTWYM-GTQSQPQRTFPEIQRRDSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 193.5; DB 4
Pred. No. 3.1e-07;
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01-DEC-2001
01-DEC-2001
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
T-cell surface glycoprotein CD4 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chan S.W.S. Middleton D.L., Lundqvist M., Warr G.W., Higgins D.A.; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF318701; AAK59279.1; -.

InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.

Pfam; PF00047; 1g; 4.

SMART; SM00409; IG; 3.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
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                                                                                                                                                             HVVKLTISSNGYFLPGDDLELTVMHKSPKSQPRFSITLFNSHNSRVTPEVLQNETPQ---
                                                                                                                                                                                                                                                                     ILAGK---IFKGRAPMSDRSET-----NQNSKHLKVSNLRISDAGTYICECGSDRNSISL
                                                                                                                                                                                                                                                                                                                             ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                        ---KYALKVKQLQPTDSGTWICNMHSDSPSINENISFNVKVL-----GFEKTHLERM
                                                                                                                                                                                                                                                                                                                                                                                RAVFVLLQLGL--THIMAHQQQIGVEGKEVILNC---KKHDKDVTWKYEYDAGSSAIIIQ
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                                                                                                          IQGGKTLSVSQLELQDSGTWTCTVLQN----QKKVEFKIDIVPCPAPEPKSCDKTH----
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TCP----ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
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54624 MW;
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Pred. No. 5.7e-07;
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SEQUENCE
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Q90524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 2.
SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antigen receptor (Fragment).
Ginglymostoma cirratum (Nurse shark).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
Elasmobranchia; Ginglymostoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Greenberg A.S., Flajnik M.F.;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Greenberg A.S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A new antigen receptor gene family that undergoes extensive somatic diversification in sharks.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 374:168-173(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Spleen;
MEDLINE=95183140; PubMed=7877689;
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FISSUE=Spleen;
                                                        114
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  364 VEWESNGQP-ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
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                                                     LEELDWIYVYGGGTGVTVNPGIPLSPPIVSLLHSATEEQRANGFVQLVCLISGYYPENIA
                                                                                                                                                                   TISKGGRYVETVNSGSKSFSLRIND-------LTV-----EDSGTYRCKVYRKNWAYDCG
                                                                                                                                                                                                                                                                                                                               PSVFLFPPKPKDTLMISRTPE------VTCVVVDVSHEDPEVKFNWYVDG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268
29579 MW;
                                                                                                                                                                                                                                                                                                                                                                                                           6.9%;
                                                                                                                                                                                                                                                                      TARVDQTPQEITKETGESLSINCVLRDSNCALPSTYWNRKKSGSTNEE
                                                                                                        ISKAKGOPREPOVYTL--PPSRDELTKNOVSLTCLVKGFYPSDIA
                                                                                                                                                                                                                                                                                                                                                                                     39;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 186; DB 13, Pred. No. 4.4e-07
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RESULT
Q8N355
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Arakawa T., Gawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashizaki Y.,
                                                                                                                                                                                                            Matches
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Best Local
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                                                                                                                                                                                                                                                                              Pfam; PF00047; 1g; 1.

SMART; SM00407; IGC1; 1.

PROSITE; PS0035; IG_LIKE; 1.

PROSITE; PS00250; IG_MHC; 1.

SEQUENCE 130 AA; 14253 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL, AK007622; BABES142.1; -.
PIR; S22760; S22760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9D8W4;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P01842; 7FAH.
MGD; MGI:1916426; 1810027001Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Pancreas; MEDLINE=21085660; PubMed=11217851;
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                                                                                                      384
                                                                                                                                                                                                              38,
                                                                                                                                                                                                                               Similarity
                                                                                                    DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
                                                                                                                                                           GQPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVL
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36.5%;
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Last annotation update)
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                                                                                                                                                                                                          Score 183.5; DB
Pred. No. 2.5e-07
8; Mismatches 4
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                438197975E766E54 CRC64;
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                                                                                                                                                                                                                                          DB 11; Length
                                                                                                                                                                                                            43;
                                                                                                                                                                                                            Indels
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                                                                                                                                         84
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RESULT Q99M11 ID Q99M11 ID Q99M11 Q99M11 Q99M11 Q99M1 Q99M1 Q99M1 Q99M1 Q0T Q1M1 Q0T M1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ঠ
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Best Local S
Matches 55
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Ro
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Q99M11;
01-JUN-2001
01-JUN-2001
01-OCT-2003
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Q8N355;
01-OCT-2002
01-OCT-2002
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SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                 Strausberg R.;
Submitted (JAN-2001)
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Mammalia; Eutheria;
                                                                                                   EMBL; BC002129; AAI
HSSP; P01703; 7FAB
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50835; IG_LIKE; PROSITE; PS00290; IG_MHC;
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                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FISSUE=Brai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKTISKAKGOPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APVLVVYDDSDRPSGIPERFSGSNSGNTATLTISRVDAGDEADYYCQLWDSSSDHPVVFG
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                                     IPR007110;
IPR003006;
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(TrEMBLrel.
(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Primates;
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Rodentia;
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Ig-like.
Ig_MHC.
Ig_v.
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25.0%; Pred. No. 5.8e-07;
tive 39; Mismatches 99
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Last sequence update)
Last annotation update)
                                                                                                                                                                        EMBL/GenBank/DDBJ databases
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WEDLINE-22388257; PubMed=12477932;

A Straubberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

A Hopkins R.F., Jordan H., Moore T., Max R., Rubin G.M., Hong L.,

A Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Wadin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Hopkins R.M., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Hopkins R.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Holting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Korzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Korzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Best Local S
Matches 58
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Q7Z3Y4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_KHC; 1
PROSITE; PS00290; IG_MHC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein. Homo sapiens (Human).
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 Submitted (MAR-2001) to the EMEMBL; BC005332; AAH05332.1; -.
Hypothetical protein.
SEQUENCE 236 AA; 25702 MW;
                                                       Strausberg R.;
Submitted (MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
                                                                                             rissue=skeletal muscle;
                                                                                                                                                                                    Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                  EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGSCAQLV-----LTQPSSVST-SLGSTAKLPCKASTGNIGDSYV--NWYQQYMGRSPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVETTQPSKQNNNKYMASSYLTLTAKAWETHSSYSCQVTHE----GHTVEKSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEKTISKAKGOPR-EPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOP-EN
                                                                                                                                                                      cDNA sequences."
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                                                                                                                                                    Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.8%; Score 183.5; DB 24.9%; Pred. No. 5.9e-07
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                                                         EMBL/GenBank/DDBJ databases
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                                                                                                                                                      99:16899-16903 (2002)
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 7FBFE4ED23084BC6
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Best Local Similarity
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01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Human esophagus tumor;
Poustka A., Albert R., Moosmayer P., Schupp I., Wellenre
Mewes H.W., Weil B., Amid C., Osanger A., Pobo G., Han M
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX537992; CAD97951.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical SEQUENCE 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical popuration DKFZP686A05192
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01-OCT-2003 (TrEMBLrel.
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EWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK
                                                                                                                                                                                                     EDPEVKFNWYVDGVEVHNAKTK--PREE----QYNSTYRVVSVLTVLHQDWLNGKEYKCK
                                                                                                                                                                                                                                                              EFK----SGAGTELSVRAKPSAP-VVSGPAARATP-----QHTVSFTCESHGFSP
                                                                                                                                                                                                                                                                                                              EFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----QYKSYPVTF--------
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                                                   VAHVTLQGDPLRGTANLSETIRVPPTLEV-TQQPVRAE----NQVNVTCQVRKFYPQRLQL
                                                                                                 VSNKALPA-PIEKT--ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAV
                                                                                                                                                       RD--ITLKWFKNGNELSDFQTNVDPAGDSVSYSIHSTAKVVLTREDVHSQVI-----
                                                                                                                                                                                                                                                                                                                                                               GPGRELIYNQKEGHFPRVTTVSDLTKRNNMDFSIRISNITPADAGTYYCVKFRKGSPDHV
                                                                                                                                                                                                                                                                                                                                                                                                                GQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQ--NQKKV
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nilarity 23.8%;
Conservative 54
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398 AA; 43260 MW; DF82E30734B1246F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 181.5; DB 4
Pred. No. 1.8e-06;
4; Mismatches 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 182; DB 4;
Pred. No. 7.8e-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158;
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3., Han M., Wiemann
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                                                                                                                                                                                                                                                                                                       Matches
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Best Local
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SMART; SM00409; IG; 6.

SMART; SM00408; IGC2; 6.

SMART; SM00137; MAM, 1.

PROSITE; PS50835; IG_LIKE; 6.

PROSITE; PS50060; MAM 2; 1.

PROSITE; PS50069; NITROGENASE 1 1; 1.

Glycoprotein; Immunoglobulin domain.

SEQUENCE 955 AA; 105790 MW; BD41A1E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002
01-OCT-2002
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF478693; AAM77220.1; -.
Genew; HGNC:19267; MGCA1.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016163; F:nitrogenase activity;
GO; GO:0009399; P:nitrogen fixation; IEJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR008957; FN III-like.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig.c2.
InterPro; IPR000998; MAM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oncogene 21:3089-3094(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             De Juan C., Iniesta P., Gonzalez-Quevedo R., Moran A., Sanchez-Pernaute A., Torres A.J., Balibrea J.L., Diaz-Rubio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=22077705; PubMed=12082541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycosyl-phosphatidyl-inositol-MAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8NFP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 6.
Pfam; PF00629; MAM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000998; InterPro; IPR000318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94
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                          SVQC-----RSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQN----
                                                                                                 KLKNLRPQDYASYTCQVSVRNVCGIPDKAITFRLTNTTAPPALK-LSVNETLVVNPGENV
                                                                                                                                                 -IKNIKIEDSDTYICEVEDQKE---EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSP 151
                                                                                                                                                                                                                                                  TVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLI 95
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                                                                                                                                                                                                TVFLRCTVNSNPPARFIWKRGSD------TLSHSQDNG-VDIYEPLYTQGETKVL
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(TrEMBLrel. 22, Last sequence up)
(TrEMBLrel. 25, Last annotation
                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                               Score 181.5; DB 4
Pred. No. 6.2e-06;
5; Mismatches 151
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RESULT
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Q8BLX5;
01-MAR-2003
01-MAR-2003
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SMART; SM00407; IGC1; 2.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG LIKE;

SEQUENCE 379 AA; 42409 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003 (TrEME Weakly similar to 9930027N05RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL, AK040982; BAC30768.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Aorta, and MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:2444824; 9930027N05Rik.
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                                                                                                                                                                                                                                                                                                                                                                              Local
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LELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPK
                                                                                                                                                                                   NSNQIKILGNQGSFLTKGPSKLNDRAD-SRRSLMDQGNFPLIIKNLKIEDSDTYICEVED
                                                                                                                                                                                                                                                          IPHCVLLLILLLGLKGAAVRELKVIQPVKSFFVGAGGSATLNCTVTYLLPVGPIKWYRGV
                                                                                                                                                                                                                                                                                                       VPFRHLLLVLQLALLPAATQGNKVVLGKK-----GDTVELTCTASQKKSI----QFHWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
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                                                    QRG-----
                                                                                                    QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQ
                                                                                                                                                      GOSRLLIYPFTGEYF----PRITSVSDVKKRSNLD---FSIRISNVTPADSGTYYC-VKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHEALHNHYTOKSLSLSPGLOLDETCAEAQDGEL
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
lar to signal-regulatory protein beta-1
                                                                                                                                                                                                                                                                                                                                                           Conservative
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                6.7%;
                                                    -SSEPDIEIOSGGGTELSVFAKP-SSPMVS--GPAARAVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW.
ω
                                                                                                                                                                                                                                                                                                                                                   70;
                                                                                                                                                                                                                                                                                                                                                         Score 181; DB 11;
Pred. No. 1.9e-06;
0; Mismatches 155
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                             055BAE20759CF6D5
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Matches 88
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INTERPRO; IPR007110; IG-lİKE.
INTERPRO; IPR003597; IG_C1.
INTERPRO; IPR003597; IG_V.
Pfam; PF00047; IG; 3.
SMART; SM004067; IGC1; 2.
SMART; SM004067; IGC1; 2.
SMART; SM004067; IGV; 1.
PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 397 AA; 44157 MW; EIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8BFX8;
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Weakly similar to signal-regulatory protein beta-1
9930027005RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hean-
9930027N05Rin.
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK036935; BAC29645.1; -.
EMBL; AK054545; BAC25818.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Ovary, and MEDLINE=22354683; PubMed=12466851; The FANTOM Consortium,
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                                                                                                                                                                                                                    88;
                                                                                                                                                                                                                                  Similarity
                         LELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPK 233
                                                                              QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQ
                                                                                                         GOSRLLIYPFTGEYF----PRITSVSDVKKRSNLD---FSIRISNVTPADSGTYYC-VKF
                                                                                                                                  NSNQIKILGNQGSFLTKGPSKLNDRAD-SRRSLWDQGNFPLIIKNLKIEDSDTYICEVED
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                                                                                                                                                                                                                    Conservative
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                                                    ----SSEPDIEIQSGGGTELSVFAKP-SSPMVS--GPAARAVP-----
                                                                                                                                                                                                                               6.7%; Score 181; DB 11; Length 397; 20.1%; Pred. No. 2e-06;
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SMART; SM00406; IG; 1.

PROSITE; PS00178; AA TRNA LIGASE_I; 1.

PROSITE; PS50835; IG_LIKE; 2.

PROSITE; PS00290; IG_MIC; 1.

Hypochetical protein.

SEQUENCE 233 AA; 24802 MW; C694F8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC007782; AAH07782.1; -.
PIR; S12440, S12440.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004812; F:tRNA ligase activity; IEA.
GO; GO:0006418; F:amino acid activation; IEA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (MAY
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InterPro; IPR001412; tRNA-synt_I.
211
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SYSCOVTHE 219
                                                     VFSCSVMHE
                                                                                                        ATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHR
                                                                                                                                                         VSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
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                                                                                                                                                                                                                                                                                                                             QTARITCGGSNLGSK----SVNWYQLRPGQAPILVVYENKERPAGIPERLSALTSEETAT
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                                                                                                                                                                                                                                                                    LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK--GQPR-EPQVYTLPPSRDELTKNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
                                                   415
                                                                                                                                                                                                                                                                                                                                                                                                                                   6.5%; Score 176.5; DB 4
26.5%; Pred. No. 2.2e-06;
tive 35; Mismatches 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C694F8397B27650B CRC64;
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                                                                                                                                                                                                                 150
                                                                                                           210
                                                                                                                                                                                                                                                                       347
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Early Cardiac

Allograft

databases

H.K.,

Frazier Β.

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RESULT
Q28260
ID Q2
AC Q2
AC Q2
DT 01
DT 01
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Novel antigen receptor (Fragment).
Ginglymostoma cirratum (Nurse shark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondr.
Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
Ginglymostomatidae; Ginglymostoma.
NCBI TaxID-7801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q90530,
028260;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation updat
Vascular cell adhesion molecule-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Spleen;
MEDLINE=95183140; PubMed=7877689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; 1g; 2.
SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0004872; F:receptor activity; InterPro; IPR007110; Ig-like. InterPro; IPR003597; Ig_cl. InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Greenberg A.S.;
Submitted (DEC-1994) to th
EMBL; U18687; AAB48358.1;
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A new antigen receptor gene family that extensive somatic diversification in shar Nature 374:168-173(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Greenberg A.S., Avila Flajnik M.F.;
                                                                                                      Q28260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Spleen;
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                                                                                                                                          99
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nes 64; Conserv
                                                                                                                                                                                                                                                427
                                                                                                                                                                                                                                                                                         173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSVFLFPPKPKDTLMISRTPE------VTCVVVDVSH-----ED
                                                                                                                                                                                                                                                                                       KNTKTITSGFATTSPVKTSSNDFSCASLLKVPLQEWSRGSVYSCQVSHSATSSNQRKEIR
                                                                                                                                                                                                                                                                                                                             SNGQP-ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
                                                                                                                                                                                                                                                                                                                                                                      YAACGAGTAVTVN--PGIPPSPPIVSLLHSATEEQRANRFVQLVCLISGYYPENIAVSWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NISPGGRYVETVNSVQNLLINDLTVEDGGTYRCGGSL----YNW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEVKFNWYVDGV-EVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
                                                                                                                                                                                                          STS
                                                                                                                                                                                                                                                SLSPGLQLDETCAEAQDGELDGLW
                                                                                                                                                                                                                                                                                                                                                                                                            ----APIEKTISKAKGOPREPOVYTL--PPSRDELTKNOVSLTCLVKGFYPSDIAVEWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259
259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.5%;
nilarity 24.2%;
Conservative 3:
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                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TARVDQTPRSVTKETGESLTINCVLRDASYALGHTCWFRKKSGSTKEE
                                                                                                                                                                                                          EIAVLLRDPTVEEIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28245 MW; 07F9860A92318B6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 176.5; DB 13; Pred. No. 2.5e-06;
                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 103; Indels
                                                                                                                                                                                                                                              450
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sharks.";
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                                                                                                      739
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                     update)
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  RESULT 100
Q63669
ID Q63669
AC Q63669
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Best Local Sin
Matches 111;
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PRINTS; PR01471; ICAMVCAM1.

PRINTS; PR01474; VCAM1.

SMART; SM00408; IGC2; 4.

PR0SITE; PS50835; IG_LIKE; 5.

Immunoglobulin domain.

SEQUENCE 739 AA; 81412 MW
  Q63669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U32086; AAA84866.1; -.
HSSP; P19320; IVCA.
GO; GO:0016020; C: membrane; IEA.
GO; GO:0016337; P:cell-cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Ballantyne C.M., Clubb F.J.,
Youker K.A., Smith C.W., Entr
Willerson J.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003987; ICAM VCAM-1
InterPro; IPR007110; Ig-Tke.
InterPro; IPR003989; Ig-cz.
InterPro; IPR003989; VCAM-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arteriopathy in the Dog.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Increased Expression of VCAM-1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9615;
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                                                                                                                           667
                                                                                                                                                                 409
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                                                                                                                                                                                                                                              350
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                                                                                                                                                                                                                                                                                                                               296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331 VVLTCGVTDCESPSFSWRTQIDSPLSGTVKVEGAKSTLTLSPVNLENEHSYLCTVTCGHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 KKGDTVELTCTASQKKSIQFHWK---NSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 6.5%; Score 176.5;
Similarity 21.9%; Pred. No. 1.1¢
11; Conservative 65; Mismatches
                                                                                                                                                               SCSVMHEALHNHYTQKSLSLSPGLQL
                                                                                                                                                                                                                                            LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS-DGSFFLYSKLTVDKSRWQQGNVF
                                                                                                                                                                                                                                                                                                                           QDWLNGKEYKCKVSNKA--LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-----VS
                                                                                                                                                                                                                                                                                                                                                                                                              PEVTCVVVDVS - - - HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS - - - VLTVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFLEDMDKKSLETKSLEMTFIPTTEDTGKVLVCLAKLHIDEMEFEPKQRQSTQTLYVNVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -FL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVE--FKIDIVPCPA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTLTLESPPGSSPS-----VQCRSPRG--KNIQGGK-TLSVSQLELQDSGTWTCTVLQNQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGNATLTLIAMRLEDSGTYVCEGVNEVGKDGKEVELIVQEKPFTVEISPGPQIIAQIGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGNFPLIIKNLKIEDSDTYIC----EVEDQKEEVQLLV----FGLTANSDTHLLQ--GQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEGGSVTMTCASEGLPPPQIFWSKKLDNGNLQLL---
                                                                                                                         ECESKNEA---
                                                                                                                                                                                                                                                                                       AKMEDSGIYVCEGINQAGISRKEVELIIQVA---PKDIQLIAFP---SESVKEGDTVIIS
                                                                                                                                                                                                                                                                                                                                                                      PRDTTVVVSPSSIVEEGSPVNMTCSSDGLPAPNILWSRRLS--NGRLQSLSEDPILTLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLEKGIKVDLYSFPRDPEVEMSGLLVDGNPVTVSCEVPNVYPSDRLEIELFKGETIIESK
                       PRELIMINARY;
                                                                                                                                                                                                          GNVPKTWII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ
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                       PRT;
                                                                                                                       -GLQL
                                                                                                                                                                                                          LKKKAETGDTVLKSRDGAY-
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Indels 167; Length

Gaps

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Best Local Similarity
Matches 101; Conserv
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GO; GO:0016037; P:cell-cell adhesion; IEA.
InterPro; IPR003987; ICAM VCAM-1.
InterPro; IPR003987; IGAM VCAM-1.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; VCAM-1.
Pfam; PF00047; Ig; 5.
PFAM; PF00047; IG; 5.
PRINTS; PR01472; ICAMVCAM1.
PRINTS; PR01474; VCAM1.
SMART; SM00408; IGc2; 4.
SMART; SM00408; IGC2; 4.
Immunoglobulin domain; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
SEQUENCE
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STRAIN-Sprague Dawley; TISSUE=Lung;

MEDLINE=92305064; PubMed=1377031;

Williams A.J., Atkins R.C., Fries J.W., Gimbrone M.A.Jr.,

Cybulsky M.I., Collins T.;

"Nucleotide sequence of rat vascular cell adhesion molecule-1 cDNA.";

Biochim. Biophys. Acta 1131:214-216(1992).

EMBL; X63722; CAA45254.1; -.

HSSP, P19320; IVCA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01.NOV-1996 (TrEMBLrel. 01, Created)
01.NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Vascular cell adhesion molecule 1 precursor.
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                                                                                                             PTPKIL--WSRQLKNGELQ------PLSQNTTLSFWATKM------EDSGIYVCEGIN
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                                                                                                                                                                           YPSDIAVEWE----SNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
                                                                                                                                                                                                                                       ME-SEPKQRQSTQTLYVNV------APKEPTIWVSPSPVPEE--GSPVNLTCSSDGF
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                                                        EALHNHYTQKSLSL----SPGLQL------DETCAEAQDGELDGLW 450
EA---GISKKSVELIIQGSSKDIQLTVFPSKSVKEGDTVIISCTCGSVPEIW 632
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739 AA;
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Search completed: August 3,

2004, 13:13:56

Job time : 42.157 secs

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Result
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          Query
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   SEQUENCE (MYELOMA PROTEIN NIE).

MEDLINE=77070269; PubMed=826475;

A PONSTING1 H., Hilschmann N.;

A PONSTING1 H., Hilschmann N.;

T'The rule of antibody structure. The primary structure of a "The rule of antibody structure. The protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).

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SEQUENCE (MYELOMA PROTEIN KOL); AND DISULFIDE BONDS.

MEDLINE=83289131; PubMed=6884994;

X MEDLINE=83289131; PubMed=6884994;

Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;

T'Three-dimensional structure determination of antibodies. Primary
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PO1857;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-MAR-2004 (Rel. 43, Last annotation
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MEDLINE=82274338; PubMed=6287432;
Ellison J.W., Berson B.J., Hood L.E.;
"The nucleotide sequence of a human immunoglobulin Nucleic Acids Res. 10:4071-4079(1982).
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Edelman G.M.;
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MEDLINE=71064025; PubMed=5530842;
Rutishauser U., Cunningham B.A.,
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MEDLINE=71064024; PubMed=5489771;
Cunningham B.A., Rutishauser U., Gall W
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Mammalia; Eutheria;
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W., Hilschmann N.;
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This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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Deisenhofer J.;
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Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
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MEDLINE=81208100; PubMed=7236608;
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MIM; 147100; -.

GO; GO:0005624; C:membrane fraction;
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InterPro; IPR007110; Ig-like.
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K -> R (IN G1M(3) MARKER).

/FTId=VAR_003886.

D -> E (IN G1M(NON-1) MARKER).
/FTId=VAR_003887.

L -> M (IN G1M(NON-1) MARKER).
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quadruplication of a 15-amino acid residue basic unit.";
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"Primary structure of human gamma 3 immunoglobulin deletion gamma 3 heavy-chain disease protein Wis.";
Biochemistry 19:4304-4308(1980).
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Proc. Natl. Acad. Sci.
-!- SUBUNIT: Dimer lin
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Mammalia; Eutheria; Primates;
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MEDLINE=77118561; PubMed=402363;
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21-JUL-1986
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MISCELLANEOUS: The hinge region in gamma-3 times as long as in other gamma chains and times as long as in other gamma preceded by a
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MISCELLANEOUS: Disease protein ZUC of the CH1 region, and part of the
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MISCELLANEOUS: The heavy chain disease properties of residues
                           segment (12-28).
                                                                                                                                                                                                                                             Natl Acad Sci U.S.A. 79:3260-3264(1982). SUBUNIT: Dimer linked by 12 disulfide bonds; interchain disulfide bond at position 7 in ad
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gion (Heavy chain dise
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Catarrhini; Hominidae; Homo.
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Best Local
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GO; GO:0003823; F:antigen binding; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_C1.
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HSSP; P01857; 1FC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                 DISULFID
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DPEVQFKWYVDGVQVHNAKTKPREQQFNSTFRVVSVLTVLHQNWLDGKEYKCKVSNKALP
         DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
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llarity 88.2%;
Conservative
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Pred. No. 1.5e
L3; Mismatches
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F -> Y (\overline{I}\overline{N} OMM).
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QV -> EB (IN ZUC).
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E69CBC95705B2F46
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N (IN OMM).
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Y (IN OMM).
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"Comparison of the hinge-coding segments heavy chain genes and the linkage of the genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986
21-JUL-1986
16-OCT-2001
                                                                                                                                    Hofmann T., Parr D.M.;
"A note of the amino acid sequence immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
                                                                                                                                                                                                                                  SEQUENCE OF 238-275 (ZIE).
MEDLINE=80114419; PubMed=118920;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN MEDLINE=80001357; PubMed=113060; Connell G.E., Parr D.M., Hofmann T.; "The amino acid sequences of the three heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang A.-C., Tung E., Fudenberg H.H.; "The primary structure of a human IgG2 heavy evolutionary, and functional implications.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure of human immunoglobulin evolution of a gene family."; Cell 29:671-679(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Linkage and sequence homology of two human immunoglobulin gamma
  SEQUENCE OF 1-121 (DOT)
                                              Submitted (MAR-1980)
                                                                  REVISIONS TO Hofmann T., 1
                                                                                                                                                                                                                                                                                                         domains of a human 1gG2 myeloma pr
Can. J. Biochem. 57:758-767(1979).
                                                                                                                                                                                                                                                                                                                               domains of a human
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MEDLINE=83001943; PubMed=6811139;
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Proc. Natl. Acad. Sci. U.S.A. 79:1
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SMART; SM00407; IGc1; 2
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Genew; HGNC:5526; IGHG2.
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PIR; A93906; G2HU.
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Frangione B., Milstein C., Pink J.R.L.;
"Structural studies of immunoglobulin G.";
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MEDLINE=72033500;
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PROSITE; PS00290; IG_MHC; 2.
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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GO:0005624; C:membrane fraction; NA
GO:0003823; F:antigen binding; TAS.
GO:0006955; P:immune response; NAS.
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KDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLT
                       KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
                                                                                                            TWTCTV-----LQNQKKVEFK--IDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKP
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REMOVED POST-TRANSLATIONALLY (PROBABLE)
S -> A (IN MYELOMA PROTEINS TIL & ZIE).
/FTId=VAR_003889.
C -> S (IN REF 3)
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HINGE.
CH2.
                                                                                                                                                                    Pred.
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Pred. No. 2.5
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DOMAIN 221
DISULFID 14
DISULFID 17
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MEDLINE=83157104; PubMed=6299662;
Ellison J.W., Buxbaum J.N., Hood L.E.;

"Nucleotide sequence of a human immunoglobulin CDNA 1:11-18(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GC4_HUMAN STANDARD; PRT; 3
P01861;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The by non-profit institutions as permedified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                          SMART; SM00407; ĬĠc1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 2.
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GO; GO:0003823; F:antigen binding; TAS.
GO; GO:0006955; P:immune response; NAS.
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PDB; 1ADQ; 16-SEP-98.
Genew; HGNC:5528; IGHG4.
MIM; 147130; -.
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Mammalia; Eutheria;
                                                                                                                                                      InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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P01730;
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SEQUENCE
               SEQUENCE FROM N.A., AND VARIANT TRP-265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      surface
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-NOV-1988 (Rel. 09,
10-OCT-2003 (Rel. 42,
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Green E.D., Dickson M.C., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Jeneration and initial analysis of more than 15,000 full-length R.D. Foc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                                                                    Nature
                                                                                                                                     human CD4."
                                                                                                                                                                                MEDLINE=97311402; PubMed=9168119;
                                                                                                                                                                                                                                       Nature
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"Cloning and sequences of primate CD4 molecules: diversity cellular receptor for simian immunodeficiency virus/human
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R MIM; 18940; ...

R GO; GO:0042101; C:T-cell receptor complex; NAS.

R GO; GO:0015026; F:coreceptor activity; NAS.

R GO; GO:0015026; F:coreceptor activity; NAS.

R GO; GO:0015029; F:thrternalization receptor activity; TAS.

R GO; GO:0004289; F:mHC class II protein binding; NAS.

R GO; GO:0004289; F:transmembrane receptor activity; TAS.

R GO; GO:0004508; F:transmembrane receptor activity; TAS.

R GO; GO:000405; F:pathogenesis; TAS.

R GO; GO:000405; F:pathogenesis; TAS.

R GO; GO:000407; F:T-cell differentiation; NAS.

R GO; GO:000407; F:T-cell differentiation; NAS.

R GO; GO:0007129; F:T-cell differentiation; NAS.

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R GO; GO:0007129; F:T-cell differentiation; NAS.

R GO; GO:0007159; F:Transmembrane receptor protein tyrosine kin...

R InterPro; IPR000973; CD4 TCA9.

R InterPro; IPR000973; CD4 TCA9.

R InterPro; IPR003596; Ig_v.

R FAINTS; PR00652; CD4TCANTIGEN.

R PRNST; SM00406; IGV; 1.

R PROSSITE; PS50035; IG_LIKE; 1.
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EMBL; U5160; AAA16069.1; -
EMBL; BC025782; AAH25782.1;
PIR; A90872; RWHUT4.
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3; 1CDJ; 31-APR-94.
3; 3CD4; 31-OCT-93.
3; 1CDJ; 01-APR-97.
4; 1CDJ; 01-APR-97.
4; 1CDJ; 01-APR-97.
4; 1WBR; 12-MAR-97.
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SUBCELULAR LOCATION: Type I membrane protein.
SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
DATABASE: NAME-PROW; NOTE=CD guide CD4 entry;
WWW#-"http://www.ncbi.nlm.nih.gov/prow/cd/cd4.htm".
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IG-LIKE C2-TYPE 1.
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/FTId=CAR_000053.
N-LINKED (GLCNAC. .
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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GO:0042109; F:GO:receptor activity; ISS.
GO:0042209; F:MC class II protein binding; ISS.
GO:0006955; P:immune response; ISS.
GO:0045086; P:positive regulation of interleukin-2 biosyn.
GO:0045087; P:T-cell differentiation; ISS.
GO:0045088; P:T-cell selection; ISS.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P03987;
23-0CT-1986 (Rel. 02, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-3 chain C region, membrane-bound form
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 3.
SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG LIKE; 3
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J00451; AAB59655.1;
EMBL; V01526; CAA24767.1;
PIR; A02156; G3MSM.
HSSP; P01857; 1FC1.
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MEDLINE=85027161; PubMed=6092053;

Wels J.A., Word C.J., Rimm D., Der-Balan

Tucker P.W., Blattner F.R.;

"Structural analysis of the murine IgG3 c

EMBO J. 3:2041-2046(1984).
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InterPro; IPR003597;
InterPro; IPR003006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane; Alternative
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                    QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                            LGGPSVELFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
QYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPI
                                                                                       LGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREA
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; Ig_MHC.
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Pred. No. 4.7e
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HINGE.
CH2.
CH3.
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CYTOPLASMIC (POTENTIAL)
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E -> Q (IN REF. 2).
P -> F (IN REF. 2).
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(See http://www.isb-sib.ch/announce/
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RESULT 8
GC1M_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Ig gamma-1 chain C region, membrane-bc
Mus musculus (Mouse)
EMBL; V00793; CAA24172.1; -. EMBL; V00793; CAA24173.1; -. EMBL; V00793; CAA24174.1; -. PIR; B02159; GIMSM.
                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Eventhe European Bioinformatics Institute. There are no restrue by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         "Gene segments encoding transmembrane immunoglobulin gamma chains."; Cell 26:19-27(1981).
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Rogers J., Choi E.,
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MEDLINE=82197626; PubMed=6804950;
Tyler B.M., Cowman A.F., Gerondakis S.D.,
"mRNA for surface immunoglobulin gamma ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma
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Honjo T., Obata M., Yamawaki-Kataoka
Takahashi N., Mano Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved transmembrane sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and complete nucleotide sequence gamma 1 chain gene."; Cell 18:559-568(1979).
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                   Name=Membrane-bound;
                                                                                                                                                                                                                                                Event=Alternative splicing;
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                                                                                                                                                                            IsoId=P01868-1; Sequence=External;
Note=May be the major isoform;
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, PubMed=6799207;
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region, membrane-bound for
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and a 28-residue
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RESULT 9
CD4_MACFA
ID CD4_M
AC P79IE
DT 15-JU
DT 10-OC
DE T-Cel
DE T4/Le

CD4_MACFA STANDARD; PRT; 458 AA. P79185; P15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) T-cell surface glycoprotein CD4 precursor (T-cell surface T4/Leu-3).

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SMART; SM00407; IGc1; 2.

PROSITE; PS50835; IG_LIKE; 3

PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Alternative splicing; Transmembrane; 3D-structure.
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MGI:96446; Igh-4
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                                                                ISKUDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNS
                                                                                                                                TKVDKKIVPRDCGC-KPCIC----TVPEV---SSVFIFPFKPKDVLTITLTPKVTCVVVD
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                GLQLDETCAEAQDGELDGLWTT 452
                                               QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
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                                QPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSP
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IPR003597; Ig_cl.
IPR003006; Ig_MHC.
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29-DEC-99.
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Pred. No. 1.4e-52;
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HSSP; P01730; IMBR.
GO; GO:0042101; C:T-cell recep
GO; GO:0015026; F:coreceptor a
GO; GO:0015026; F:mHC class II
GO; GO:0006955; P:immure respo
GO; GO:0045058; P:positive reg
GO; GO:0045058; P:T-cell diffe
GO; GO:0045058; P:T-cell gelec
GO; GO:0045058; P:transmembran
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SEQUENCE
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Tatsumi M., Yabe M., Yamada Y.K.;
Tatsumi M., Yabe M., Yamada Y.K.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
I to the EMBL/GenBank/DDBJ databases.
I antiger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00692; CD4TCANTIGEN SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin domain;
                                                                                                                                             Local Sin
hes 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO:0042101; C:T-cell receptor complex; ISS.
GO:0015026; F:coreceptor activity; ISS.
GO:0042289; F:MC Class II protein binding; ISS.
GO:0006955; P:immune response; ISS.
GO:0045086; P:positive regulation of interleukin-2 biosyn.
GO:0030217; P:T-cell differentiation; ISS.
GO:0045088; P:T-cell selection; ISS.
GO:007169; P:transmembrane receptor protein tyrosine kin.
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SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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                                                                     MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                            MNRGI PFRHLLLVLQLALLPAVTQGKKVVLGKKGDTVELTCNASQKKNTQFHWKNSNQIK
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158
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79.6%;
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
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4; Mismatches
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Pred. No. 1.
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les 28;
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(By similarity)
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GO; GO:00042289;
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15-JUL-1998
15-JUL-1998
10-OCT-2003
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
-i- SUBUNIT: Associates with p56-lck (By similarity).
-i- SUBCELULUAR LOCATION: Type I membrane protein.
-i- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-i- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                             SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca fuscata fuscata (Japanese macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Cercopith
                                                                                                                                                                          PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell;
Immunoglobulin domain; Signal; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T-cell surface glycoprotein CD4 precursor (T-cell surface antigen T4/Leu-3).
                                                                                                                                                                                                                                                                                                            InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003506; Ig_v.
Pfam; PF00047; ig; 2.
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Hashimoto O., Tatsumi
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                                                                                                                                                                                                                                                           ; PR00692; CD47
SM00406; IGV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  P:positive regulation of interleukin-2 biosyn. . P:T-cell differentiation; ISS.
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                                                                                                                     EXTRACELLULAR
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                                                                                                                                             GLYCOPROTEIN
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Best Local S
Matches 175
EMBL; J00471; AAB59661.1; A
PIR; A02154; G2MSAM.
PDB; 1KB5; 08 APR-98.
PDB; 1YEB; 15-OCT-97.
MGD; MGI:96443; Igh-1.
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                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig gamma-2A chain C region, membrane-bound form.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin gamma chains.
Proc. Natl. Acad. Sci. U.S.I
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Yamawaki-Kataoka Y., Nakai S., Mi
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                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P01864-1; Sequence=External;
Note=Probably the major isoform;
SIMILARITY: Contains 3 immunoglobulin-like domains.
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Rodentia;
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Pred. No. 4.6e-51;
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Matches 173
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InterPro; IPR003006; Ig_MHC.
Pfam; pF00047; ig; 2.
SWART; SW00407; IGC1; 2.
SWART; SW00407; IGC1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS508290; IG_MHC; 1.
                                                                                                                                     CD4 MACMU STANDARD;
P1603; 029617;
P1603 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
10-CCT-2003 (Rel. 42, Last annotation update)
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NON TER 1
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TRANSMEM
DOMAIN
CARBOHYD
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SEQUENCE FROM N.A.

MEDLINE-90.182664; PubMed=2107024;
Camerini D., Seed B.;
"A CD4 domain important for HIV-mediated outside the virus binding site.";
Cell 60:747-754(1990).
[2]
                                                                          Macaca mulatta (Rhesus macaque).

Bukaryota; Metazoa; Chordata; Craniata; V.

Mammalia; Eutheria; Primates; Catarrhini;

Cercopithecinae; Macaca.

NCBI_TaxID=9544;
                                                                                                                                    T-cell surface glycoprotein T4/Leu-3).
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73; Conservative
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IPR003597; Ig_c1.
IPR003006; Ig_MHC.
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CYTOPLASMIC (POTE
N-LINKED (GLCNAC
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1; Mismatches
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Pred. No. 6.
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i; Cercopithecidae;
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HLIM)
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                             syncytium
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mangabeys (Primates: Papionini).";

Mol. Biol. Evol. 15:892-900(1998).

Hol. Biol. Evol. 15:892-900(1998).

Hol. Biol. Evol. 15:892-900(1998).

Hol. Biol. Evol. 15:892-900(1998).

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                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00692; CD4TC;
SMART; SM00406; IGv; 1
PROSITE; PS50835; IG_L:
                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000973; CD4 TCA9;
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig v.
Pfam; PF00047; ig; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93049640; PubMed=1425921;
Fomsgaard A., Hirsch V.M., Johnson P.R.;
"Cloning and sequences of primate CD4 molecules: diversity of the
cellular receptor for simian immunodeficiency virus/human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hashimoto O., Tatsumi M.;
"Molecular cloning and expressions the Submitted (JUN-1995) to the [3]
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TISSUE=Thymocytes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunodeficiency virus.";
Eur. J. Immunol. 22:2973-2981(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 28-424 FROM
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                                                                                                                                                                                                                                                                                                                                        mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0042101; C:T-cell receptor complex; ISS.
GO:0015026; F:coreceptor activity; ISS.
GO:00150289; F:MHC class II protein binding; ISS.
GO:00042289; F:Mmune response; ISS.
GO:0006955; F:Immune response; ISS.
GO:0045086; P:positive regulation of interleukin-2 biosyn.
GO:0030211; P:T-cell differentiation; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO:0045058; P:T-cell selection; ISS. GO:0007169; P:transmembrane receptor
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o the EMBL/GenBank/DDBJ databases
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                                                                                                                    POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
BY SIMILARITY
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BY SIMILARITY
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S-palmitoyl cysteine (
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Best Local
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15-JUL-1998 (Re
10-OCT-2003 (Re
T-cell surface (
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Q08340; P
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                             -!- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
-!- SUBUNIT: Associates with p56-lck (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                            Fomegaard A., Hirsch V.M., Johnson P.R.; Cloning and sequences of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIPID
                                                                                                                                                     immunodeficiency virus.";
Eur. J. Immunol. 22:2973-2981(1992).
                                                                                                                                                                                                              MEDLINE=93049640; PubMed=1425921;
                                                                                                                                                                                                                             TISSUE=Blood,
                                                                                                                                                                                                                                                                          Hashimoto
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                          Macaca nemestrina
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(Rel. 36, Last sequence update,
(Rel. 42, Last annotation upda
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a license agreement (See http://www.isb-sib.ch/announce,
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rsor (T-cell surface
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